EXHIBIT 10

AVITI

Rapid insights with affordable sequencing at any scale

Watch Video >

Explore Datasets >

Rewrite the future of genomics

AVITI is a benchtop sequencing instrument with reimagined core technology to deliver flexibility and affordability while setting the standard for data quality. An alternative model, AVITI LT, is a lower cost, lower throughput solution that brings innovative next-generation sequencing (NGS) to more labs.

Flexible throughput

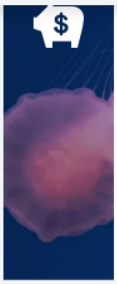
Scale run output to suit virtually any application, without waiting or paying more.

Unprecedented quality

Leverage exceptional accuracy with ≥ 70% Q50 and ≥ 90% Q40 data (when using Cloudbreak UltraQ).

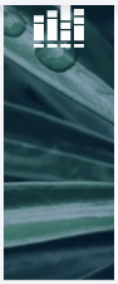
Independent flow cells

With a dual flow cell layout and individually addressable lanes, you can perform two parallel runs and operate each side independently.



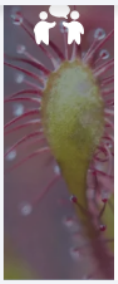
Ultimate affordability

Extend your budget with industry-low sequencing costs and fixed reagent prices.



End-to-end workflows

Enjoy simple, complete workflows from library prep to analysis solutions.



Dedicated support

Rely on a smooth installation process and scientist-to-scientist converstaions.

Powered by ABC sequencing

We innovated the core components of sequencing to introduce a radically new way of generating genomics data while reducing run costs and improving performance.

- Avidite base chemistry (ABC) circularizes, copies, and rolls each strand into tightly bound polonies without the use of PCR.
- Fluorescent avidites bind to each polony creating ultrastable complexes. Low-binding surface chemistry makes the signal prominent for highly-accurate detection.
- Rolling circle amplification (RCA) avoids index hopping and other PCR-induced errors while ultratight complexes reduce reagent consumption.
- The inherent flexibility of these methods establishes a strong foundation for continued performance and capability gains.

Download Infographic

Always the right fit

Whether you need 2 billion reads per run or 100 million, one AVITI powers a wide range of experiments. Fully saturate two high-output flow cells to maximize your capacity or load one lane of a single low-output flow cell.

- No need to batch smaller experiments with precision pricing.
- Comprehensive sequencing kits run any read length from 2 x 75 to 2 x 300.
- Low-, medium-, and high-output kit options dial in a precise number of reads while maintaining affordability.
- Individually addressable lanes confine a library pool to one lane for project separation and maximum multiplexing.

View Animation

Seamless Library Compatibility

Cloudbreak Freestyle™

Cloudbreak Freestyle sequencing kits ensure seamless integration with your current sequencing workflows. Compatible with our Elevate™ workflow and most third-party libraries, you can directly load linear libraries onto the AVITI, without manual library conversion.

Learn More >

Elevate Workflow

The Elevate Workflow prepares libraries from input DNA for sequencing on AVITI. Equipped with 96 unique dual indexes optimized for color balance, this native library prep solution facilitates whole-genome sequencing and is adaptable to other applications.

Learn More >

Adept Workflow

The Adept Workflow makes any prepared library compatible with AVITI. Designed for simplicity, this adaptation solution capitalizes on our unique combination of cost, performance, and flexibility while maintaining your favored library prep and analysis.

Learn More >

AVITI LT

Offering the same technology and features as AVITI, AVITI LT provides an ABC sequencing solution to suit your budget. The only difference is throughput: AVITI LT is limited to low- and medium-throughput capabilities with the flexibility to upgrade to a full-throughput AVITI with a simple software update.

Resources

View Virtual Demo

Download Brochure

View Specifications

Start your AVITI journey

Get in Touch

First Name *

Last Name *

Email

Company Name *

Phone

Select a State *

Zip Code

United States

Job Function

Cancer

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Your Science Can't Wait

Have a question?

Contact Us

Document title: Element AVITI System Sequencing Instrument | Element Biosciences
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Capture timestamp (UTC): Tue, 18 Feb 2025 19:00:50 GMT

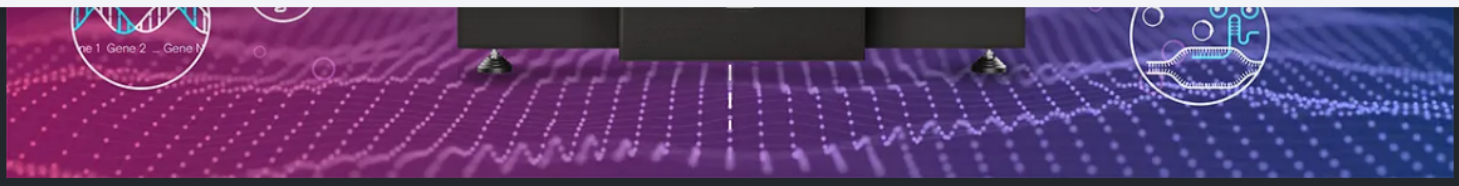
EXHIBIT 11

AVITI 24

Next gen sequencing meets in situ multiomics

Speak to an expert ›

One instrument, infinite discoveries



AVITI24 is the first benchtop platform to enable high-quality, affordable sequencing and in situ multiomics in one powerful system. From exome sequencing to spatial proteomics, AVITI24 empowers endless possibilities for biological discovery on a single, integrated platform.

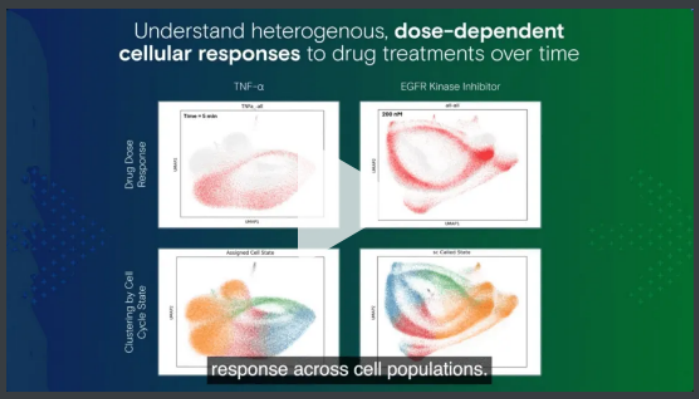
Learn more about Cloudbreak sequencing >

Learn more about Teton CytoProfiling >

A new era in cellular mapping

Teton CytoProfiling empowers researchers to unravel the complexities of cellular function with precise spatial detection of RNA, proteins, and cell morphology—all in one high-resolution platform. With integrated multiomic analysis from Teton, you can explore cellular phenotypes, decode signaling pathways, and uncover cellular heterogeneity driving disease.

Learn more about Teton CytoProfiling >



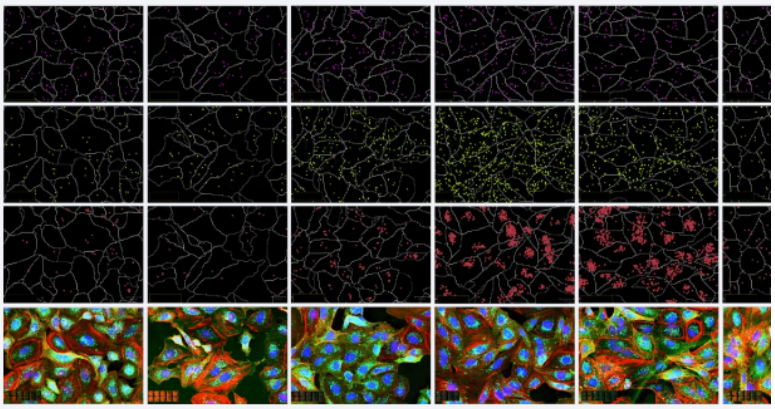
Unlocking new insights into the biology of drug response

Watch Video ›

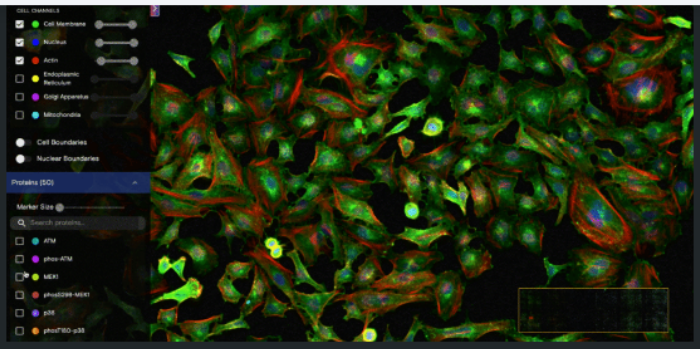
Accelerate discoveries with next day results

AVITI24 Teton CytoProfiling is designed for scale—profiling up to 2 million cells across dual flow cells with 20 cm^2 of total imageable area. Unlock multiomic data with less than 1 hour of hands-on time and next day results.

Learn more about the AVITI24 ›



Visualize biology in new ways



Onboard primary analysis automates data processing, so your data is ready as soon as a run is complete. Explore cells with CytoCanvas or seamlessly integrate Teton data with community-developed tools for downstream analysis.

Resources

Download Brochure

Read Blog Post

Download Spec Sheet

Start your AVITI24 journey

Get in touch

First Name *
Last Name *
Email *
Company Name *
Phone
Select a State *
Zip Code
United States
Job Function
Cancer
How Can We Help You?

I would like to speak with an Element Specialist.
I want to stay up-to-date with the latest Element news.

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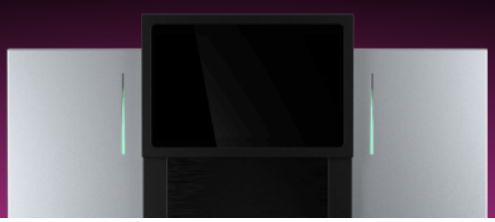
Your Science Can't Wait



Have a question?

Contact Us ›

Email *

Company Name *

Phone

Select a State *

Zip Code

United States

Job Function

Cancer

How Can We Help You?

☐ I would like to speak with an Element Specialist.

☐ I want to stay up-to-date with the latest Element news.

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Your Science Can't Wait

Have a question?

Contact Us ›

EXHIBIT 12

Element Biosciences

Specification Sheet

Element AVITI24™ System

In situ multiomics and next-generation sequencing on a single platform with unmatched performance and limitless possibilities

Highlights

- Analyze RNA, protein, and morphology in a single sample
- Profile up to 1 M cells in one run with next-day results
- Capture transcripts and proteins with sensitivity and specificity
- Prepare cell samples in 45 minutes hands-on time

Introduction

One integrated biology platform, the AVITI24 System seamlessly combines best-in-class sequencing with in situ multiomics. Teton™ CytoProfiling simultaneously measures multiple molecular features in up to 1 million cells per flow cell for deep multiomic profiling of adherent cells or cell suspensions. From a single sample, you can analyze RNA, proteins, and cell morphology with next day results. On the same system, the AVITI24 delivers high-quality next-generation sequencing (NGS) with uncompromising performance, flexibility, and affordability, and access to assays from whole-genome sequencing to targeted panels.

Multiomics unleashed by ABC

Avidite base chemistry (ABC), breakthrough optical design, image processing algorithms, and flexible surface chemistries, enable high-plexity multiomic analysis directly in intact cells. Teton chemistries for RNA, protein, and cell paint analysis use probe or antibody-mediated detection schemes coupled with ABC sequencing to measure RNA and protein expression at subcellular resolution in individual cells. Proprietary cell paint profiling provides visualization of the cell membrane, nucleus, and mitochondria, as well as other cell organelles.

Cell segmentation is performed using cell paint features coupled with machine learning models validated on diverse cell types, ensuring accurate transcript and protein assignment to the correct cell.

The AVITI24 can detect thousands of transcripts per cell and billions of high-quality transcripts in situ on one Teton flow cell for sensitive detection of genes across a range of expression levels, fueling high-resolution cell typing and pathway analysis.

Figure 1. AVITI24 unites the diverse worlds of molecular biology and cell imaging on one compact benchtop system.

Industry-leading throughput

The AVITI24 technology is designed for more cells, more samples, and more experiments, empowering transformative discoveries without constraints. With an imaging area of 10 cm² and dual flow cell architecture, the AVITI24 is capable of profiling up to 2 million cells per run, scaling the number of samples, conditions, or perturbations possible in a single run.

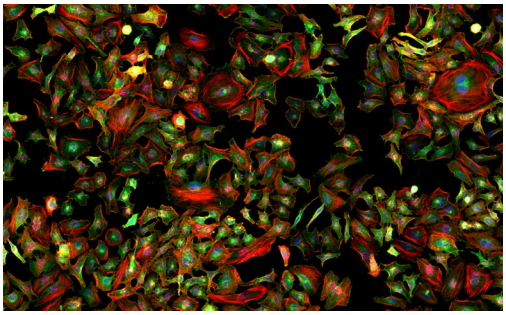

Figure 2. Cell paint on AVITI24 using ABC sequencing readout.

The off-instrument workflow requires 45 minutes of hands-on time to prepare your cells and assemble the flow cell. Probe hybridization or antibody binding, amplification, and sequencing occur directly onboard the instrument. Analyte detection is enabled by direct sequencing of AVITI barcodes, which obviates the need for time-consuming decoding steps.

The AVITI24 software suite includes real-time, onboard cell segmentation, cell assignment, and morphology reporting to accelerate downstream data analysis.

Teton flow cells are available as either ready-to-use PLL-coated flow cells or uncoated customizable flow cells to support a broad range of cell types and culture conditions. The AVITI24 launches with two fixed Teton 350-plex RNA and 50-plex protein panels focused on deep profiling of the MAPK signaling pathway for cell cycle and apoptosis regulation in human samples. The expanding AVITI24 roadmap includes additional fixed and custom panels with expanded plexity, and direct in situ sequencing for targeted or untargeted transcriptome analysis to accelerate discovery power.

Summary

From deciphering cellular development to uncovering drug resistance mechanisms, AVITI24 expands scientific possibilities by harnessing the power of cell imaging and multiomics in one instrument. With a streamlined workflow and industry-leading runtime, the AVITI24 accelerates the pace of scientific discovery and reimagines what is possible from a single benchtop system.

System specifications

Instrument Configuration	Dual flow cells AVITI Operating Software Ubuntu Core 20.04 LTS operating system
Operating Environment	Temperature: 18°C to 26°C Elevation: < 2000 m Sound level: ≤ 62 db at 3.3 ft
Instrument Dimensions	(H x W x D) 29.5 in x 37.6 in x 28.5 in Weight: 155.1 kg/342 lb
Power Requirements	100–240 VAC at 50/60 Hz 15 A, 550 W (average)

Sequencing specifications

Read Count[a]	High output: Medium output: Low output:	1.5 B reads per flow cell 750 M reads per flow cell 375 M reads per flow cell
Accuracy	> 90% Q30 with 2 x 150 and 2 x 75 cycles > 85% Q30 with 2 x 300 cycles > 70% Q50 with Cloudbreak UltraQ™ kits[c]	
Inputs	Direct loading of linear libraries with Cloudbreak Freestyle™ kits	
Run Time[b]	≤ 24 hours 2 x 75 cycles ≤ 38 hours 2 x 150 cycles ≤ 60 hours 2 x 300 cycles	

[a] Increased output available Mid 2025. Performance metrics are based on sequencing Element libraries. Actual results might differ due to library type and preparation methods.
[b] Individually addressable lanes and custom recipes can extend run times.
[c] Based on Elevate™ libraries and specific run parameters.

Cytoprofiling specifications

Analytes	RNA, protein, morphology 100 bp in situ RNA sequencing in 2025
Plex	RNA: 350 targets Protein: 50 targets Morphology: 6 markers
Content	MAP Kinase Cell Cycle and Apoptosis Immunology, neuroscience, and custom panels in 2025
Imaging	< 250 nm subcellular spatial resolution with multi-feature cell segmentation
Inputs	Adherent cells, Cell suspensions in 2025
Sensitivity	1 M mean counts detected per mm2
Throughput	Up to 1 M cells with 10 cm² area per flow cell Two flow cells per run
Format	12 wells (0.5 cm²/well) 1 well (10 cm²/well)
Run Time[a]	24 hours
Sample Prep	45 minutes

[a] Run time is based on a single 12-well run and software update available in 2025.

Ordering information

Element AVITI24 System	880-00004
Element AVITI24 Upgrade	895-00060
Teton Optimization Kit	860-00022
Teton Human MAPK & Cell Cycle Kit, 12 Well	860-00023
Teton Human MAPK & Cell Cycle Kit, 1 Well	860-00024
Teton Human MAPK & Apoptosis Kit, 12 Well	860-00025
Teton Human MAPK & Apoptosis Kit, 1 Well	860-00026
Teton, Flow Cell Assembly Kit, 1 Well (2-pack)	860-00027
Teton, Flow Cell Assembly Kit, 12 Well (2-pack)	860-00028
Teton Slide Kit, PLL - 1 Well (2-pack)	860-00029
Teton Slide Kit, Uncoated - 1 Well (2-pack)	860-00030
Teton Slide Kit, PLL - 12 Well (2-pack)	860-00031
Teton Slide Kit, Uncoated - 12 Well (2-pack)	860-00032
Teton Flow Cell Assembly Tool Set	860-00033

To learn more, visit elementbiosciences.com

Element Biosciences
Telephone: 619.353.0300
Email: info@elembio.com

EXHIBIT 13

Element Biosciences

Cloudbreak™ Sequencing

User Guide

FOR USE WITH

AVITI™ System, catalog # 880-00001
AVITI™ System LT, catalog # 880-00003
AVITI24™ System, catalog # 880-00004
AVITI Operating Software v3.3.0 or later
Cloudbreak, Cloudbreak Freestyle™, and Cloudbreak UltraQ™ Sequencing Kits

ELEMENT BIOSCIENCES
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Document # MA-00058 Rev. E
April 2025

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Table of Contents

Overview

The Cloudbreak sequencing workflow uses a Cloudbreak Freestyle, Cloudbreak, or Cloudbreak UltraQ kit to sequence libraries on an AVITI System or an AVITI24 System.

- **Cloudbreak Freestyle**—Provides multiple read lengths and output options to meet a diversity of applications. Cloudbreak Freestyle kits enable direct loading of linear libraries without library conversion, including third-party libraries.
- **Cloudbreak**—Provides the same read length and output options as Cloudbreak Freestyle with potential requirements for library circularization.
- **Cloudbreak UltraQ**—Provides high-quality Q40 and Q50 data for highly sensitive assays.

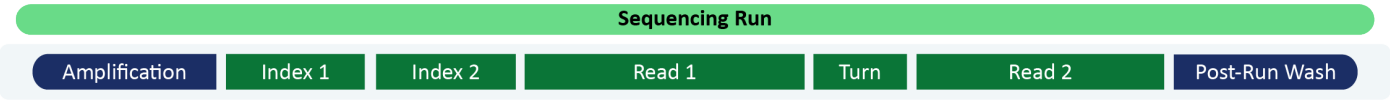
All Cloudbreak kits are designed for minimal waste and easy disposal. Reagent overage supports the extra cycles that index sequences and unique molecular identifiers (UMIs) need to identify samples with high confidence. For a list of kit configurations and catalog numbers, see *Cloudbreak Sequencing Kits* on page 23.

Cloudbreak kits are compatible with a variety of library preparation workflows. For more information on compatibility, see the *Product Compatibility* page on the Element website.

Sequencing Run Stages

AVITI Operating Software (AVITI OS) generates a recipe based on the run parameters entered during run setup. The recipe governs each stage of a run. A run is complete when the recipe is executed and primary analysis is finished. The following stages comprise a sequencing run:

- **Amplification**—Hybridizes the library to the flow cell and performs amplification to form polonies, each containing multiple copies of the same sequence from the library.
- **Sequencing**—Performs each read in the run, including imaging and primary analysis.
- **Post-run wash**—Automatically flushes buffer from the sequencing cartridge through the fluidic system to remove salts and residual library.



Reads in a Sequencing Run

Up to four reads comprise a sequencing run: Index 1, Index 2, Read 1, and Read 2.

- **Index reads**—A run can include one, two, or no index reads.
  - » **Index 1** sequences the Index 1 sequence.
  - » **Index 2** sequences the Index 2 sequence.
  - » A dual-index run sequences Index 1 and Index 2.
- **Read 1 and Read 2**—All runs must have a Read 1.
  - » **Read 1** sequences the forward strand of the DNA insert.
  - » **Read 2** sequences the reverse strand.
  - » A paired-end run sequences Read 1 and Read 2, including a paired-end turn before Read 2 to generate the complementary strand.

Run Times

Kit Configuration	Read Length	Run Time (hours)*
High output	2 x 75	24
	2 x 150	38
	2 x 300	60
Medium output	2 x 75	20
	2 x 150	31
	2 x 300	51
Low output	2 x 75	17
	2 x 150	27

* Individually addressable lanes and custom recipes can extend run times.

Read Counts and Output

Cloudbreak and Cloudbreak Freestyle Kit Configuration	Kit Size	Target Read Counts	Output (Gb)
High output	2 x 75	1 billion	150
	2 x 150	1 billion	300
	2 x 300	300 million	180
Medium output	2 x 75	500 million	75
	2 x 150	500 million	150
	2 x 300	100 million	60
Low output	2 x 75*	100 million	15
	2 x 150	250 million	75

* Available as Cloudbreak Freestyle chemistry only

Cloudbreak UltraQ Kit Configuration	Kit Size	Target Read Counts	Output (Gb)
High output	2 x 150	800 million	240

Number of Cycles

Read length is the total number of cycles performed in a run. The optimal number of cycles and how to distribute the total cycles depends on your experiment. For bioinformatics purposes, adding one extra cycle to each read is recommended. For example, a 2 x 150 cycle run ideally includes 2 x 151 cycles. The additional cycle improves the accuracy of the Q score for the 150th cycle.

The software and chemistry used for the run prescribe a minimum number of cycles. Read 1 requires at least five cycles and at least 25 cycles to generate all run metrics. The maximum number of cycles depends on the kit:

- A 2 x 75 kit performs up to 184 cycles, supporting one 2 x 76 run with indexing and unique molecular identifiers (UMIs).
- A 2 x 150 kit performs up to 334 cycles, supporting one 2 x 151 run with indexing and UMIs.
- A 2 x 300 kit performs up to 634 cycles, supporting one 2 x 301 run with indexing and UMIs.

Library Considerations

Some libraries have special considerations for sequencing. Make sure to follow the applicable requirements for your library.

Low-Diversity Amplicon Libraries

For low-diversity, high-multiplex libraries, such as a 16S amplicon library, Element recommends that you enable the Low-Diversity High-Multiplex setting during run setup. This setting requires a library pool that meets the following requirements:

- Adept™ libraries or third-party libraries
- High plexity of ≥ 64 unique dual indexed (UDI) libraries
- A 1–5% spike-in of PhiX Control Library

CAUTION
Exceeding a 5% spike-in can reduce the index diversity of the pool, leading to a reduction in quality.

Bead-Based Normalization

PCR is required when sequencing a library pool that has undergone the bead-based normalization protocol. Before diluting to the target loading concentration, use amplification and Qubit kits to amplify and quantify the library pool.

- For Cloudbreak chemistry with Adept libraries, use the Adept Rapid PCR-Plus Kit for amplification.
- For Cloudbreak Freestyle chemistry with third-party libraries, use the KAPA HiFi HotStart Library Amplification Kit with Primer Mix. Follow manufacturer instructions.

Short Insert or Long Insert Libraries

Sequencing short insert or long insert libraries require that you specify the preloaded custom recipe during run setup.

Short insert libraries	If you are using Cloudbreak Freestyle chemistry and libraries with < 100 bp inserts, the short insert recipe is required. For libraries with 100–300 bp inserts, the short insert recipe is recommended. For more information, see *Sequencing Short Insert Libraries with Cloudbreak Freestyle*. The short insert recipe is compatible with 2 x 75 and 2 x 150 kits.
Long insert libraries	If you are using Cloudbreak or Cloudbreak Freestyle chemistry and libraries with > 750 bp inserts, the long insert recipe is required. The long insert recipe is compatible with 2 x 75 and 2 x 150 kits. Using a 2 x 300 kit accounts for long insert conditions.

Input Recommendations

The recommended input for sequencing is ≥ 1 nM library. The input library is normalized to 1 nM, denatured into single strands, and diluted to the target loading concentration. When starting with a 0.2–1 nM library, the library is denatured and diluted but not normalized. Library pools that start at < 0.2 nM are not supported.

PhiX Control Library Spike-In

For most applications, Element recommends a spike-in of PhiX Control Library. The following recommendations for spike-in percentages optimize the benefits of PhiX Control Library for specific experiments.

Experiment	Spike-In (%)
QC and error rate reporting	> 2
Low-complexity indexing (≤ 2-plex)	> 2
Libraries that use Low-Diversity High-Multiplex setting	1–5
Other low-diversity libraries*	≥ 5

* For Adept and third-party workflows, the first four cycles of Read 1 require high diversity. Index 1 includes high diversity for Elevate™ workflows.

Custom Primers

You can sequence any combination of I1, I2, R1, and R2 custom primers for third-party libraries with Cloudbreak Freestyle chemistry and Adept libraries with Cloudbreak chemistry. The custom primers must be HPLC-purified and prepared using the applicable method:

- **Spike-in**—Spike-in custom primers into the Cloudbreak Freestyle cartridge or the Adept Primer Set Cloudbreak tubes.
- **Replacement**—Replace the primers in the cartridge with buffer tubes from the Custom Primer Set Cloudbreak Freestyle or Adept Custom Primer Set Cloudbreak and add custom primers.

Sequencing Primer Compatibility

- For Cloudbreak Freestyle chemistry, Element oligonucleotides include sequencing primers that are compatible with standard Nextera, TruSeq, and small RNA libraries.
- For original Cloudbreak chemistry, sequencing primers are only compatible with standard Nextera and TruSeq libraries.
- Libraries with sequencing primer binding sites that do not meet these requirements *must* use custom primers.

Custom primers require special consideration and planning. To determine if your library requires custom primers and ensure a run with custom primers meets specifications, contact Element Technical Support early in experiment planning. For more information on Cloudbreak Freestyle custom primer recommendations, see *Cloudbreak Freestyle Compatibility with Third-Party Libraries*.

Loading Concentration

Use the following recommendations as a starting point to determine your optimal loading concentration. Recommendations are based on libraries prepared for Element and depend on your chemistry, kit size, library prep workflow, and other lab-specific factors. Some libraries require a higher or lower concentration than the indicated ranges.

Library size refers to the full length of the library, including the DNA insert and adapters. If you are sequencing pooled libraries, the pool must contain libraries with similar size distributions.

Loading concentration recommendations depend on your kit chemistry, output level, and size. Polony counts increase as the loading concentration increases. Lower polony counts promote higher data quality but lower the amount of data output.

Cloudbreak Chemistry, 2 x 75 and 2 x 150 Kits

Average Library Size	Adept v1.1	Adept Rapid PCR-Plus	Elevate PCR-Free	Elevate PCR-Plus
Small (250–450 bp)	4–6 pM	10–14 pM	6–10 pM	8–11 pM
Medium (450–700 bp)	6–10 pM	10–14 pM	7–11 pM	9–12 pM
Large (≥ 700 bp)	10–14 pM	10–14 pM	7–11 pM	9–12 pM

Cloudbreak Chemistry, 2 x 300 Kits

Average Library Size	Adept v1.1	Adept Rapid PCR-Plus	Elevate PCR-Free	Elevate PCR-Plus
Medium (450–700 bp)	4–6 pM	5–8 pM	3–5 pM	4–6 pM
Large (≥ 700 bp)	6–8 pM	5–8 pM	3–5 pM	4–6 pM

Cloudbreak Freestyle Chemistry, 2 x 75 and 2 x 150 Kits

Average Library Size	Elevate PCR-Free	Elevate PCR-Plus	Third Party PCR-Free	Third Party PCR-Plus
Small (250–450 bp)	5–9 pM	7–10 pM	6–9 pM	7–10 pM
Medium (450–700 bp)	6–10 pM	8–11 pM	7–10 pM	9–12 pM
Large (≥ 700 bp)	6–10 pM	8–11 pM	7–10 pM	9–12 pM

Cloudbreak Freestyle Chemistry, 2 x 300 Kits

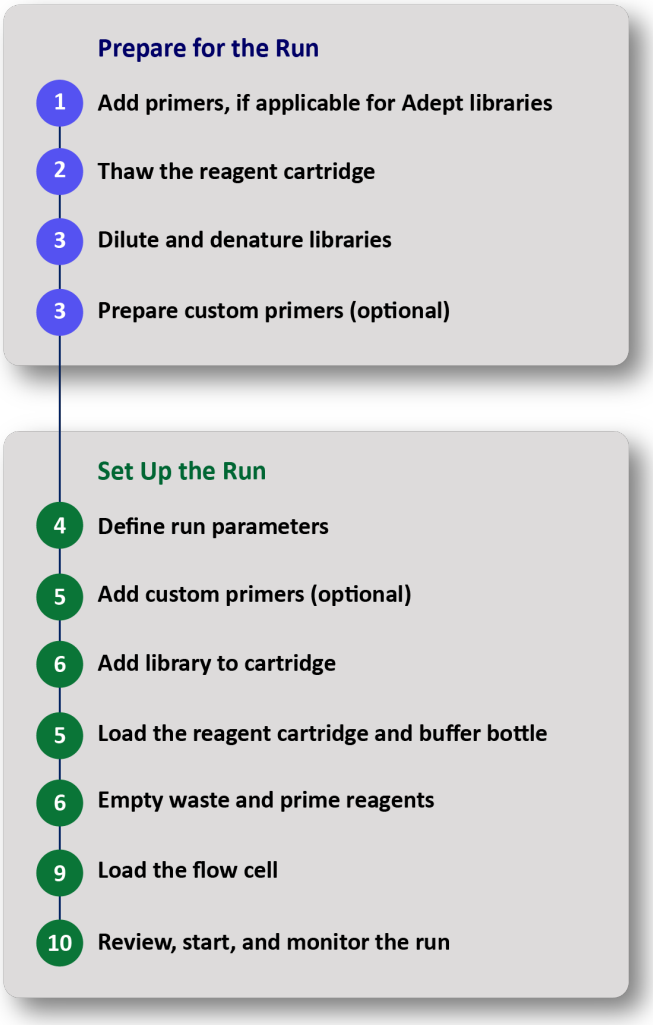
Average Library Size	Elevate PCR-Free	Elevate PCR-Plus	Third Party PCR-Plus	Third Party PCR-Free
Medium (450–700 bp)	3–5 pM	4–8 pM	6–9 pM	4–6 pM
Large (≥ 700 bp)	3–5 pM	4–8 pM	8–12 pM	4–6 pM

Cloudbreak UltraQ Chemistry, 2 x 150 Kit

Average Library Size	Elevate Libraries
450–550 bp	5–6 pM

Cloudbreak Workflow Summary

Performing a Cloudbreak sequencing run includes steps to prepare reagents and dilute the library to the appropriate volume and concentration for sequencing. For more information, see *Loading Concentration* on page 8.



Run Preparation

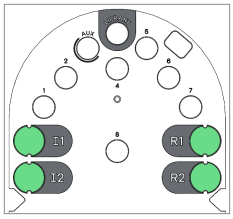
Run preparation includes adding appropriate primers, if applicable, and thawing the sequencing cartridge. The subsequent dilution procedure includes the option to store a normalized library. If you intend to store a library, do not prepare the cartridge until you are ready to sequence. Prepare the cartridge within a day of sequencing.

Add Primer Tubes

1. If you are using a Cloudbreak Freestyle sequencing kit without custom primers *or* you are sequencing Elevate libraries, skip the following steps and proceed to *Thaw Reagents* on page 10.
2. Remove a cartridge and applicable primer set from -25°C to -15°C storage.

Chemistry and Library	Primer Strategy	Primer Set
Cloudbreak, Adept	No custom primers	Adept Primer Set Cloudbreak
	Custom primers (spike-in method)	Adept Primer Set Cloudbreak
	Custom primers (replacement method)	Adept Custom Primer Set Cloudbreak
Cloudbreak Freestyle, Third Party	Custom primers	Custom Primer Set Cloudbreak Freestyle

3. Twist the primer tubes in wells labeled I1, I2, R1, and R2 toward the left to unlock.



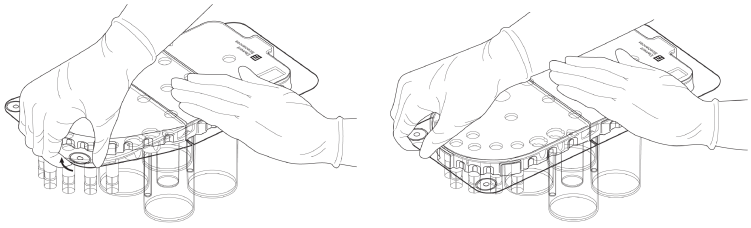
4. Remove the primer tubes from the cartridge and discard per the SDS.

   If you have trouble removing the tubes, peel the labels off and twist the tubes as you push upwards.
5. Insert the tubes from the primer set into the vacated wells. Match the abbreviation on the tube label to the well label.
6. Twist each tube right until it locks into place.

Thaw Reagents

1. If the cartridge includes a shipping cover, remove the shipping cover:

   a. While supporting the cartridge, lift the removal tab at the left corner until it releases from the cartridge.



   b. Moving across the front edge of the shipping cover, repeatedly lift the edge until the cover is fully released.

   c. Pull to remove the remainder of the shipping cover from the cartridge.
2. Thaw the sequencing cartridge. Protect the cartridge from light until loading onto the instrument.

Cartridge	Room Temperature Water Bath	Refrigerator
2 x 75	90 minutes	8 hours
2 x 150, 2 x 300	2.5 hours	24 hours

3. Make sure reagents are *fully* thawed. Inspect each well as reagents thaw at varying rates.
4. If any ice remains, continue thawing.
5. Set aside the thawed cartridge at room temperature. If you do not immediately initiate the run, place the thawed cartridge at 2°C to 8°C. You can store overnight for use the next day.
6. Proceed to *Run Setup* on page 13.

Dilute Library and Custom Primers

The library dilution procedures prepare 1.4 ml diluted library at the target loading concentration with an optional spike-in. Custom primers are diluted as applicable. If you are using the Individually Addressable Lanes add-on, follow the applicable procedures for both libraries. Both libraries use the same denature and dilution methods, resulting in a total volume of 1.4 ml for each library.

Prepare the Library

For bead-normalized libraries, perform amplification and quantification before proceeding. See *Bead-Based Normalization* on page 6.

1. Gather the following consumables:
   - » 0.2 M Tris-HCl buffer, pH 7.0
   - » 1 N NaOH
   - » 2 ml DNA LoBind tubes (4–7)
   - » 10 mM Tris-HCl, pH 8.0 with 0.1 mM EDTA (low TE buffer)
   - » Nuclease-free water
2. Combine the following reagents to prepare 0.2 N NaOH. Use 0.2 N NaOH within the day and discard.

Reagent	Volume
1 N NaOH	20 µl
Nuclease-free water	80 µl
Total	**100 µl**

3. Remove the following components from -25°C to -15°C storage and thaw on ice:
   - » Library Loading Buffer
   - » Experimental library
   - » [Optional] PhiX Control Library
4. Pulse vortex the thawed libraries and briefly centrifuge.
5. If the experimental library is ≥ 1 nM, normalize:
   a. In a new DNA LoBind tube, use low TE buffer to dilute the library to 1 nM.
   b. Proceed immediately or cap the tube, store the 1 nM library at -25°C to -15°, and sequence within the allotted time.

Denature the Library with NaOH

1. Calculate the loading concentration of each library, experimental and control, based on the target loading concentration and relative amount of each library:

$$loading\ concentration\ in\ pM = target\ loading\ concentration\ in\ pM * library\ amount\ in\ \%$$

—For example, if the target loading concentration is 9 pM with a 2% spike-in: the experimental library concentration is 8.82 pM (9 pM * 98%) and the control library concentration is 0.18 pM (9 pM * 2%).—

NOTE
The experimental and control library concentrations do not need to match.

2. Calculate the experimental library volume based on the calculated loading concentration and a 1.4 ml loading volume:

$$library\ volume\ in\ \mu l = (library\ loading\ concentration\ in\ pM * 1400\ \mu l)/library\ starting\ concentration\ in\ pM$$

—Continuing the preceding example and assuming a 1 nM starting concentration, the library volume is 12.3 µl: (8.82 pM * 1400 µl)/1000 pM.—

3. If you are adding a spike-in, calculate the control library volume based on the loading concentration and a 1.4 ml loading volume:

$$control\ library\ volume\ in\ \mu l = (control\ library\ loading\ concentration\ in\ pM * 1400\ \mu l)/control\ library\ concentration\ in\ pM$$

—Continuing the preceding example and assuming a 1 nM PhiX Control Library, the control library volume is 0.25 µl: (0.18 pM * 1400 µl)/1000 pM.—

4. If the volume calculated in step 3 is < 1 µl, dilute PhiX Control Library in low TE buffer to use a volume ≥ 1 µl for accurate pipetting.
5. Record the total volume of diluted sequencing library (experimental and control) in µl.

   —This procedure uses equal volumes of library, 0.2 N NaOH, and 0.2 M Tris-HCl buffer, pH 7.0. Therefore, the volume recorded at this step is used in two subsequent steps.—
6. Combine the library volumes calculated in steps 2 and 3 in a new DNA LoBind tube.
7. Add an equal volume of freshly prepared 0.2 N NaOH.
8. Vortex the tube to mix and briefly centrifuge.
9. Incubate the tube at room temperature for 5 minutes to denature the library.
10. Vortex the tube to mix and briefly centrifuge.
11. Add 0.2 M Tris-HCl buffer, pH 7.0 at an equal volume of 0.2 N NaOH to neutralize the reaction.
12. Vortex the tube to mix and briefly centrifuge.

    —The library is denatured, neutralized, and at 1/3 the input concentration in 3x input volume.—
13. Add a sufficient volume of Library Loading Buffer to reach a total volume of 1.4 ml:

$$buffer\ volume\ in\ \mu l = 1400\ \mu l - 3 * library\ volume\ in\ \mu l$$

14. Vortex the tube to mix and briefly centrifuge.
15. Place the diluted sequencing library on ice. Use within the day.

Prepare Custom Primers

1. If you are not using custom primers, skip the following steps and proceed to *Run Setup* on page 13.
2. In a new DNA LoBind tube, prepare each applicable custom primer using low TE buffer:

Custom Primer	Volume	Concentration
Index 1	19 µl	100 µM
Index 2	19 µl	100 µM
Read 1	32.4 µl	100 µM
Read 2	19 µl	100 µM

3. Set aside the 100 µM custom primers on ice. Use within the same day.

Run Setup

Run setup for sequencing prompts you to define run parameters, load sequencing consumables, and empty the waste bottle. Before initiating a run, review the overview, software, troubleshooting, and safety information in the user guide for your instrument.

Initiate a Sequencing Run

1. Gather the following materials:
   - » Buffer bottle
   - » Cartridge
   - » Cartridge basket
   - » Towel or wipe
   - » Used flow cell

   —A used flow cell might already be present on the instrument.—
2. If applicable, stage run manifests for import:
   - » If setting up the run manually, save the manifest on a USB and connect the USB drive to an instrument USB port.
   - » Alternatively, you can save the manifest to the specified SMB storage connection.
   - » If you planned the run in ElemBio Cloud, upload the manifest to the planned run.
3. On the Home screen, select **New Run**.
4. If AVITI OS prompts that the flow cell is missing, load a ***used*** flow cell:
   a. Select **Open Nest**.
   b. Place the used flow cell onto the nest and close the lid.
   c. Select **Close Nest**.
5. Select **Sequencing**.
6. Select the side for sequencing:
   - » **Side A**—Set up a run on side A.
   - » **Both**—Set up runs on sides A and B.
   - » **Side B**—Set up a run on side B.
7. For chemistry type, select **Cloudbreak**, and then select **Next**.
8. Proceed as follows:
   - » For a planned run created in ElemBio Cloud, proceed to *Select a Planned Run*.
   - » For a manual run, proceed to *Define Manual Run Parameters* on page 14.

Select a Planned Run

1. Select **Planned Run**.

   AVITI OS displays a list of compatible planned runs for the instrument and run type. For information on planned run compatibility, see *Run Planning* in the *Online Help*.
2. Select the run you want to use from the list of planned runs.
3. Review the run parameter fields to make sure they are correct.

   If you need to edit a planned run, modify it in ElemBio Cloud. See *Run Planning* in the *Online Help*.
4. In the Storage drop-down menu, select the storage connection for the run.

5. Select **Next** to proceed to the Prepare Reagents or the Run Side B screen.
   - » After you proceed, the selected planned run becomes unavailable for other connected instruments.
   - » If you exit run setup before priming, the run returns to the list of available planned runs.
6. If applicable, repeat steps 2–5 to set up a dual start run with a second planned run.
7. Proceed to *Inspect and Mix Reagents* on page 15.

Define Manual Run Parameters

1. Make sure **Manual Run** is selected for the type of run.
2. In the Run Name field, enter a unique name to identify the run.

   —The field accepts 1–64 alphanumeric characters, hyphens (-), and underscores (_).—
3. If applicable, select **Browse** and import the run manifest.
4. [Optional] In the Description field, enter a description that represents the run.

   —The field accepts ≤ 500 alphanumeric characters, hyphens, underscores, spaces, and periods (.).—
5. In the Storage drop-down menu, select a storage location:
   - » To output run data to the default storage location, leave the default selection.
   - » To override the default storage location for the current run, select a storage connection.
6. Select a Library Type:
   - » **Elevate**—Sequence libraries prepared with Elevate indexes and adapters.
   - » **Adept**—Sequence libraries prepared with the Adept Workflow. Only compatible with Cloudbreak sequencing kits.
   - » **Third Party**—Sequence libraries prepared with a third-party workflow. Only compatible with Cloudbreak Freestyle sequencing kits.
7. If applicable, select a Library Structure:
   - » **Circular**—Sequence libraries that complete circularization before loading.
   - » **Linear**—Sequence libraries prepared for on-instrument circularization.
8. In the Sequencing Kit drop-down menu, select the kit you are using. For information on kit compatibility, see the *Product Compatibility* page on the Element website.

   —The kits listed depend on compatibility with the instrument type, and the selected library type and library structure.—
9. If you are using the Adept or Third Party library type, select a Low-Diversity High-Multiplex option.
   - » **Yes**—Sequence low-diversity high-multiplex libraries. This option requires at least 4 cycles for Index 1.
   - » **No**—Sequence other libraries.
10. If you are using the Individually Addressable Lanes add-on and a compatible sequencing kit, select the number of library pools.
11. In the Cycles fields, enter the number of cycles to perform in each read.
    - » Do not exceed the maximum number of cycles for the sequencing kit. See *Number of Cycles* on page 6.
    - » Add one cycle to the desired number of Read 1 and Read 2 cycles. For example, enter **151** in the Read 1 field to perform 150 cycles in Read 1.
    - » To skip a read, enter **0**.
    - » See the following table for minimum and default cycle values. Aside from the minimum cycle limitations, AVITI OS lets you distribute the available cycles among reads as necessary.

Library Type	Kit Size	Minimum Values				Default Values			
		Index 1	Index 2	Read 1	Read 2	Index 1	Index 2	Read 1	Read 2
Adept or Third Party	2 x 75	0	0	5	0	Blank	Blank	76	76
	2 x 150	0	0	5	0	Blank	Blank	151	151
	2 x 300	0	0	5	0	Blank	Blank	301	301
Elevate	2 x 75	4	0	5	0	12	9	76	76
	2 x 150	4	0	5	0	12	9	151	151
	2 x 300	4	0	5	0	12	9	301	301

12. If you are using the Advanced Run Settings, select **Advanced Settings** and proceed to *Configure Advanced Run Settings*.
13. Select **Next** to proceed to the Run Side B or Prepare Reagents screen.
14. If applicable, repeat steps 2–13 to set up a dual start run.

Configure Advanced Run Settings

Use Advanced Run Settings to modify primary analysis and recipe configurations for a run. Available settings depend on kit compatibility. Some settings require the activation of an add-on. For more information, see the Advanced Run Settings and Add-On information in the user guide for your instrument.

1. If you are using the Polony Density setting, select a Polony Density option.
   - » **Standard**—Uses the standard read output.
   - » **High Density**—Increases the read output.
2. If you are using the Filter Mask setting, enter a base mask to use for filtering.
   - » Use the base mask format. For more information, see *Base Masks* in the *Online Help*.
   - » If you do not use the Filter Mask setting, the default filter mask is `R1:Y15N*-R2:Y15N*`.
3. If you are using the Custom Recipes setting, import the custom recipe file from preloaded recipes or a USB drive:
   a. Select **Browse**.
   b. Select **Element Recipes** for preloaded recipes or **USB** to upload from a connected USB drive.
   c. Select the recipe file, and then select **Open**.
4. If you are using the PMG Shift setting, enter the number of cycles to skip.

   You cannot skip more than 20 cycles. The number of skipped cycles reduces the maximum number of cycles AVITI OS allows for the run.
5. Select **Next** to proceed.

Inspect and Mix Reagents

1. Inspect each cartridge well to make sure reagents are fully thawed.
2. Make sure the cartridge contains the appropriate primers.
3. Make sure the tubes in the I1, I2, R1, and R2 wells are secure. If necessary, twist each tube to the right.
4. Gently invert the cartridge ***10 times*** to mix reagents.

   CAUTION
   Inadequately mixed reagents can cause run failure.

5. Tap the cartridge base on the benchtop to remove any large droplets from the tube tops.
6. Inspect the small tubes to make sure reagents are settled at the bottom.
7. Place the cartridge into a clean cartridge basket and lock the clips. Wipe any excess moisture.

Add Custom Primers to the Cartridge

1. If you are not using custom primers, skip the following steps and proceed to *Add Library to the Cartridge*.
2. Using a new 1 ml pipette tip, pierce the center of the applicable I1, I2, R1, and R2 wells to create one hole. Push the foil to the edges.
3. Discard the pipette tip.
4. Add the applicable volume of 100 µM custom primer to each pierced well.

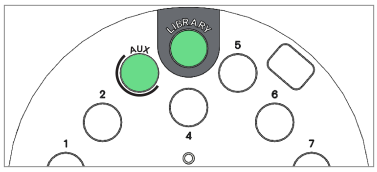
Custom Primer	Volume	Well
Index 1	19 µl	I1
Index 2	19 µl	I2
Read 1	32.4 µl	R1
Read 2	19 µl	R2

—The final concentration of each custom primer is 1 µM.—

5. Pipette the content of each tube 15 times to mix. Avoid losing existing primer volume.

Add Library to the Cartridge

1. Using a new 1 ml pipette tip, pierce the center of the Library well to create one hole. Push the foil to the edges.



2. Discard the pipette tip.
3. Briefly centrifuge the diluted sequencing library to remove bubbles and foam from the tube lid.
4. Transfer the entire volume of diluted sequencing library to the Library well, dispensing along the well wall.
   - » Avoid aspirating any foam or dispensing air.
   - » Do not allow the library to contact the foil.
   - » Make sure the tube contains ≥ 1.3 ml diluted sequencing library.
5. If you are using the Individually Addressable Lanes add-on, repeat steps 1–4 with the AUX well and the second library.

   —The library for the AUX well contains the samples for Lane 2 in the run manifest.—

   CAUTION
   Transferring a library to the AUX well of an incompatible cartridge damages the library and the cartridge. For more information on Individually Addressable Lanes add-on compatibility, see the user guide for your instrument.
6. Inspect the Library well through the window at the front of the basket.
   - » Make sure the library is free of foam and that bubbles are minimal.
   - » If an air gap appears below the surface, use a new pipette tip to remove it.
7. If the cartridge include shipping locks, twist each shipping lock left to unlock and remove them from the cartridge lid.

Confirm Reagent Preparation

1. If you selected Adept, select the **Swap primer tubes** checkbox to confirm that the I1, I2, R1, and R2 wells contain Adept primers or custom primers.
2. Select the **Invert cartridge** checkbox to confirm that reagents are mixed.
3. Select the **Insert into basket** checkbox to confirm that the cartridge is in the cartridge basket.
4. Select any load library checkboxes to confirm that the cartridge contains diluted library.
5. Select **Next** to proceed to the Load Reagents screen.

Load Reagents and Buffer

1. Open the reagent bay door.
2. Remove any materials from the reagent bay and set aside.
3. Slide the basket containing the thawed cartridge into the reagent bay until it stops.
4. Support the buffer bottle with both hands and slide it into the reagent bay until it stops.
5. Close the reagent bay door, and then select **Next** to proceed.

Empty Waste and Prime Reagents

1. Open the waste bay door.
2. Unscrew the transport cap from the cap holder above the waste bay.
3. Remove the waste bottle from the waste bay and close the transport cap.

   CAUTION
   Waste bottle contents are considered hazardous. Dispose of waste according to local, state, and regional laws and regulations.
4. [Optional] Insert a funnel into a waste receptacle. Make sure the funnel is secure.
5. Open the transport cap and the vent cap.
6. Support the waste bottle with both hands and empty the waste:

   a. Position the bottle over the funnel or waste receptacle.
      - If you inserted a funnel, align the handle to the inner edge of the funnel.
      - If you did not insert a funnel, center the handle over the waste receptacle.

   b. Tip the bottle forward and drain. Invert the bottle and shake to expel all droplets.

   c. If necessary, wipe liquid off the bottle.
7. Close the vent cap and return the empty waste bottle to the waste bay.
8. Screw the transport cap onto the cap holder and close the waste bay door.
9. Bring a new Cloudbreak flow cell to room temperature:

   a. Remove a flow cell pouch from 2°C to 8°C storage. ***Do not open the pouch.***

   b. Set aside the pouch for at least 5 minutes.

   NOTE
   Before priming, you can discard run setup and save the cartridge. Priming pierces reagent seals and prevents further use.
10. Select **Next** to ***automatically*** start priming.

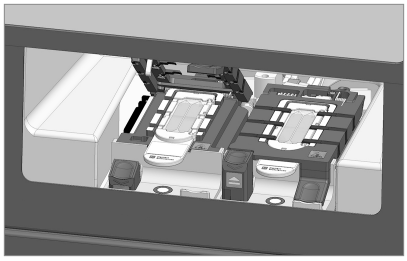
    Priming takes ~ 5 minutes or up to 8 minutes at high elevations.
11. When priming is complete, select **Next** to proceed to the Load Flow Cell screen.

    AVITI OS moves the nest forward and opens the nest bay door. A brief delay is normal.

Load the Flow Cell

1. Make sure the nest status light is blue.
2. Press the button to the left of the nest to open the lid. Failure to fully press down on the button can cause errors when closing the lid or aligning the flow cell.
3. Remove the used flow cell from the nest. Discard or store at room temperature for use with priming or washes.
4. Unpackage the new Cloudbreak flow cell. Handle the flow cell by the gripper only.

   CAUTION
   Touching the glass can introduce debris, smudges, and scratches, compromising data quality.
5. Face the label up and place the flow cell over the three registration pins on the nest.



6. Lower the tab on the right side of the lid until the lid snaps into place.
7. Select **Close Nest** to close the nest bay door and retract the stage.
8. Select **Next** to proceed to the Run Summary screen.

Review and Start the Run

1. On the Details page, review the run parameters:

Parameter	Description
Library	The workflow that prepared the libraries and the library type
Sequencing Kit	The size and version of the sequencing kit
Storage	The location where sequencing output is stored
Manifest	The file name of the uploaded run manifest, if applicable
Cycles	The number of cycles in each read
Description	An optional description of the run
Advanced	If applicable, the advanced run settings for the run

2. Review the flow cell, cartridge, and buffer bottle information:

Field	Description
Lot Number	The number assigned to the batch the consumable was manufactured with
Expires on	The year, month, and date that the consumable expires
Serial Number	The unique identifier or all zeros indicating an unscanned barcode
Part Number	The Element-assigned identifier for the consumable

3. Select **Run** to start sequencing.

4. [Optional] If you imported run manifests from a USB drive, disconnect the USB drive:
   a. In the taskbar, select **USB Drive**, and then select **Eject**.
   b. Detach the USB drive from the instrument.
5. Process the materials removed from the reagent bay:
   » For a used cartridge and buffer bottle, follow the instructions in *Discard the Cartridge and Bottle* on page 20.
   » For a wash tray, follow the guidelines in the user guide for your instrument. Residual liquid in the wash tray is normal.

Monitor Run Metrics

1. If necessary, select **Details** to open run details.
2. Monitor run metrics as they appear onscreen. AVITI OS indicates the expected cycle that metrics appear.
   —The expected cycles are approximate, and all metrics are estimates. Bases2Fastq generates the final metrics.—
3. Continue monitoring the run as AVITI OS refreshes the metrics.
   » Each cycle refreshes the Q scores, error rates, base compositions, and index metrics.
   » If you are using the Individually Addressable Lanes add-on, AVITI OS displays metrics for each library pool.
   » AVITI OS refreshes the yield and reads metrics after cycle 15 of Read 2:
      ◦ If Read 2 contains no cycles, metrics refresh after cycle 15 of Read 1.
      ◦ If Read 1 or Read 2 contain fewer than 15 cycles, metrics refresh when the last cycle begins.
4. When the run is complete, leave all materials on the instrument.
   » To return to the Details view, select **Overview**.
   » To access run data, go to your storage location.

Initiate Flexible Start

Flexible start provides the option to start a run or recovery wash while another run is in progress. AVITI OS safely pauses the run on the adjacent side.

1. On the Home screen, select **New Run**.
2. When prompted to request flexible start and pause the active run, select **New Run**.

Step	Estimated Wait Time to Pause*
Amplification	2 hours
Index 1, Index 2, Read 1, or Read 2	A few minutes
Turn	30 minutes
Wash	1 hour

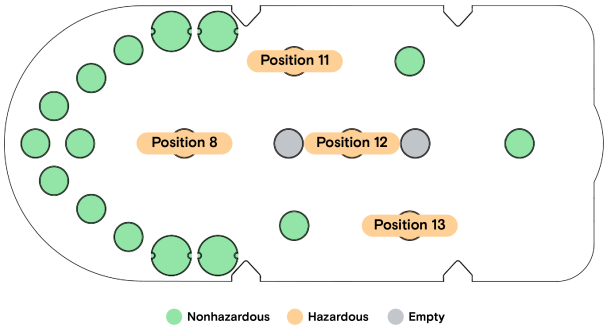
* Estimates are for 2 x 75 and 2 x 150 runs with Cloudbreak chemistry. For 2 x 300 runs, the wait time for a pause at the amplification step can exceed 2 hours.

3. Wait for the run to pause.
   » To cancel flexible start while waiting, select **Cancel Request**.
   » Contact Element Technical Support if the wait time exceeds 5 hours at the amplification step or 1.5 hours at any other step.
4. When the run pauses, proceed through run setup and start the second run or recovery wash.
   » For run setup instructions, proceed to *Initiate a Sequencing Run* on page 13.
   » For recovery wash instructions, see the user guide for your instrument.
5. To cancel setup of the second run or recovery wash, select **Back** to return to the Home screen, and then select **Resume**.

Discard the Cartridge and Bottle

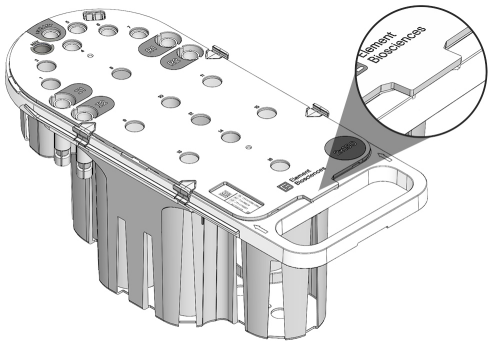
The cartridge and buffer bottle contain reagents with region-specific disposal requirements, which are described in the Safety Data Sheets (SDS) at elementbiosciences.com/resources. The amount of reagent remaining in each well after a run depends on how many cycles the run performed.

The following wells contain hazardous reagents. The position numbers in the figure align with the position numbers in the SDS.



Dispose of Reagents

1. Keep the cartridge in the basket with the clips locked.
2. Grip the lid tab and ***quickly and forcefully*** pull off the lid. Expect resistance.



3. Remove the wells indicated as hazardous from the cartridge.
   —The volume remaining in each well depends on the number of cycles performed.—
4. Using a pipette tip or a similar tool, enlarge the hole in each foil seal to form a triangle.

5. Empty each well into hazardous waste or other appropriate container per the SDS.
6. Unlock the clips and remove the cartridge from the basket.
7. Remove the remaining wells from the cartridge and enlarge the hole in each foil seal.
8. Empty each well into the appropriate container per the SDS.
9. Discard the cartridge and buffer bottle per the SDS.
10. Rinse the basket with nuclease-free water and dry upside down.

Troubleshooting

The following troubleshooting information addresses problems that can occur during run setup and sequencing with a Cloudbreak, Cloudbreak Freestyle, or Cloudbreak UltraQ kit. If a problem persists, contact Element Technical Support. For more information on troubleshooting, see the user guide for your instrument.

Run Setup Problems

Problem	Resolution
The flow cell is cracked, scratched, or otherwise damaged.	Contact Element Technical Support.
Small particulates are visible in the flow cell lane.	See *Cloudbreak Flow Cell Variations* on page 28.
The lid does not engage when a flow cell is on the nest.	Remove the flow cell and wipe the nest. Inspect the flow cell for large debris and wipe with an alcohol pad if necessary. Reload the flow cell.
AVITI OS cannot detect a loaded cartridge or waste bottle.	Follow the onscreen prompt to reload the cartridge or waste bottle. Make sure the applicable bay, reagent or waste, is unobstructed, and that the cartridge is contained within a cartridge basket.
The system cannot scan or detect a barcode on the cartridge, buffer bottle, or flow cell.	Follow the onscreen prompt to reload the consumable or continue by manually entering consumable information.
The flow cell version is incompatible with the cartridge.	Load a flow cell that is the same version as the cartridge.

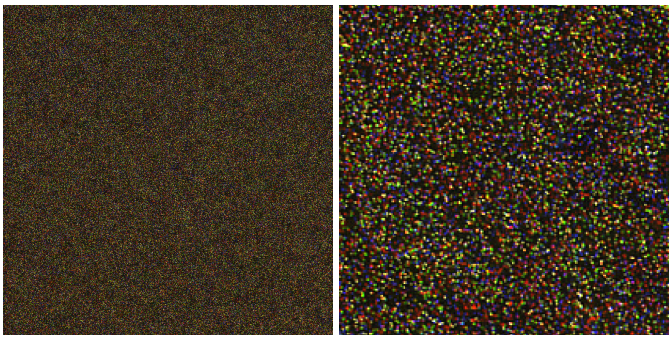
Sequencing Problems

Problem	Resolution
Polony density is lower or higher than expected.	Contact Element Technical Support or stop the run. For instructions on stopping a run, see the troubleshooting section of the user guide for your instrument.
The assigned or perfect match metrics are lower than expected.	Make sure that the index sequences recorded in the run manifest are correct.
The samples with low representation metric is higher than expected.	Select **Sample Details** to view the samples with low representation. Make sure that the index sequences recorded in the run manifest and the pooling concentration are correct.
The Q30 percentage is lower than expected.	Contact Element Technical Support.
The PhiX error rate is higher than expected.	
The flow cell contains very few polonies or no polonies.	
The user interface is frozen.	

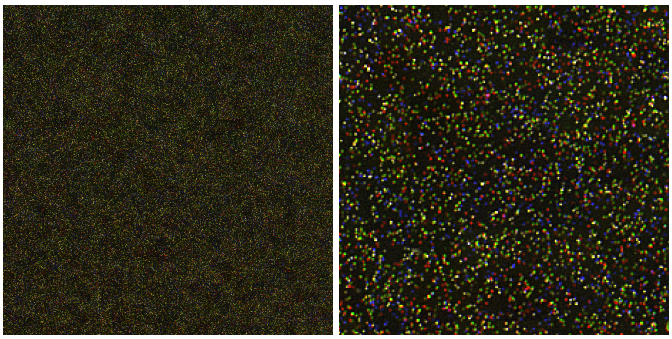
Thumbnail Image Troubleshooting

The following figures show example thumbnail images for a standard flow cell, an underloaded flow cell, and an overloaded flow cell. If the thumbnail image for a run indicates an underloaded flow cell, increase the loading concentration. For an overloaded flow cell, reduce the loading concentration. If problems persist, contact Element Technical Support.

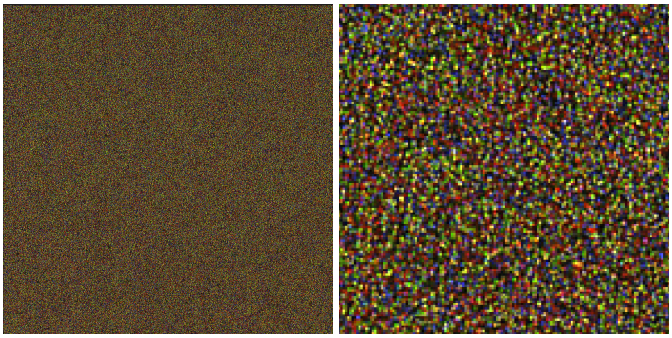
Example expected thumbnail image, full-size and zoomed



Example thumbnail image with underloading, full-size and zoomed



Example thumbnail image with overloading, full-size and zoomed



Cloudbreak Consumables

Cloudbreak consumables include a sequencing kit and optional controls and custom primers. The workflow also requires user-supplied consumables. For a list of required equipment, see the site prep guide for your instrument.

Cloudbreak Sequencing Kits

The following tables list the kit contents and storage requirements. Kits contain one of each part listed. The Library Loading Buffer pouch includes two tubes. For SDS information, see elementbiosciences.com/resources.

AVITI 2x150 Sequencing Kit Cloudbreak UltraQ, # 860-00018

Part #	Component	Shipping	Storage
820-00026	AVITI 2x150 Cartridge Cloudbreak UltraQ	-25°C to -15°C	-25°C to -15°C
810-00008	AVITI Flow Cell Cloudbreak UltraQ	Room temperature	2°C to 8°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x75 Sequencing Kit Cloudbreak Freestyle High Output, # 860-00015

Part #	Component	Shipping	Storage
820-00022	AVITI 2x75 Cartridge Cloudbreak Freestyle High Output	-25°C to -15°C	-25°C to -15°C
810-00003	AVITI Flow Cell Cloudbreak Freestyle	Room temperature	2°C to 8°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x75 Sequencing Kit Cloudbreak Freestyle Medium Output, # 860-00014

Part #	Component	Shipping	Storage
820-00021	AVITI 2x75 Cartridge Cloudbreak Freestyle Medium Output	-25°C to -15°C	-25°C to -15°C
810-00003	AVITI Flow Cell Cloudbreak Freestyle	Room temperature	2°C to 8°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x75 Sequencing Kit Cloudbreak Freestyle Low Output, # 860-00034

Part #	Component	Shipping	Storage
820-00032	AVITI 2x75 Cartridge Cloudbreak Freestyle Low Output	-25°C to -15°C	-25°C to -15°C
810-00003	AVITI Flow Cell Cloudbreak Freestyle	Room temperature	2°C to 8°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x150 Sequencing Kit Cloudbreak Freestyle High Output, # 860-00013

Part #	Component	Shipping	Storage
820-00020	AVITI 2x150 Cartridge Cloudbreak Freestyle High Output	-25°C to -15°C	-25°C to -15°C
810-00003	AVITI Flow Cell Cloudbreak Freestyle	Room temperature	2°C to 8°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x150 Sequencing Kit Cloudbreak Freestyle Medium Output, # 860-00012

Part #	Component	Shipping	Storage
820-00019	AVITI 2x150 Cartridge Cloudbreak Freestyle Medium Output	-25°C to -15°C	-25°C to -15°C
810-00003	AVITI Flow Cell Cloudbreak Freestyle	Room temperature	2°C to 8°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x150 Sequencing Kit Cloudbreak Freestyle Low Output, # 860-00011

Part #	Component	Shipping	Storage
820-00018	AVITI 2x150 Cartridge Cloudbreak Freestyle Low Output	-25°C to -15°C	-25°C to -15°C
810-00003	AVITI Flow Cell Cloudbreak Freestyle	Room temperature	2°C to 8°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x300 Sequencing Kit Cloudbreak Freestyle High Output, # 860-00017

Part #	Component	Shipping	Storage
820-00024	AVITI 2x300 Cartridge Cloudbreak Freestyle High Output	-25°C to -15°C	-25°C to -15°C
810-00003	AVITI Flow Cell Cloudbreak Freestyle	Room temperature	2°C to 8°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x300 Sequencing Kit Cloudbreak Freestyle Medium Output, # 860-00016

Part #	Component	Shipping	Storage
820-00023	AVITI 2x300 Cartridge Cloudbreak Freestyle Medium Output	-25°C to -15°C	-25°C to -15°C
810-00003	AVITI Flow Cell Cloudbreak Freestyle	Room temperature	2°C to 8°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x75 Sequencing Kit Cloudbreak High Output, # 860-00004

Part #	Component	Shipping	Storage
820-00015	AVITI 2x75 Cartridge Cloudbreak High Output	-25°C to -15°C	-25°C to -15°C
810-00002	AVITI Flow Cell Cloudbreak	Room temperature	2°C to 8°C
820-00010	Adept Primer Set Cloudbreak	-25°C to -15°C	-25°C to -15°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x75 Sequencing Kit Cloudbreak Medium Output, # 860-00007

Part #	Component	Shipping	Storage
820-00014	AVITI 2x75 Cartridge Cloudbreak Medium Output	-25°C to -15°C	-25°C to -15°C
810-00002	AVITI Flow Cell Cloudbreak	Room temperature	2°C to 8°C
820-00010	Adept Primer Set Cloudbreak	-25°C to -15°C	-25°C to -15°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x150 Sequencing Kit Cloudbreak High Output, # 860-00003

Part #	Component	Shipping	Storage
820-00013	AVITI 2x150 Cartridge Cloudbreak High Output	-25°C to -15°C	-25°C to -15°C
810-00002	AVITI Flow Cell Cloudbreak	Room temperature	2°C to 8°C
820-00010	Adept Primer Set Cloudbreak	-25°C to -15°C	-25°C to -15°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x150 Sequencing Kit Cloudbreak Medium Output, # 860-00006

Part #	Component	Shipping	Storage
820-00012	AVITI 2x150 Cartridge Cloudbreak Medium Output	-25°C to -15°C	-25°C to -15°C
810-00002	AVITI Flow Cell Cloudbreak	Room temperature	2°C to 8°C
820-00010	Adept Primer Set Cloudbreak	-25°C to -15°C	-25°C to -15°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x150 Sequencing Kit Cloudbreak Low Output, # 860-00005

Part #	Component	Shipping	Storage
820-00011	AVITI 2x150 Cartridge Cloudbreak Low Output	-25°C to -15°C	-25°C to -15°C
810-00002	AVITI Flow Cell Cloudbreak	Room temperature	2°C to 8°C
820-00010	Adept Primer Set Cloudbreak	-25°C to -15°C	-25°C to -15°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x300 Sequencing Kit Cloudbreak High Output, # 860-00008

Part #	Component	Shipping	Storage
820-00016	AVITI 2x300 Cartridge Cloudbreak High Output	-25°C to -15°C	-25°C to -15°C
810-00002	AVITI Flow Cell Cloudbreak	Room temperature	2°C to 8°C
820-00010	Adept Primer Set Cloudbreak	-25°C to -15°C	-25°C to -15°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

AVITI 2x300 Sequencing Kit Cloudbreak Medium Output, # 860-00009

Part #	Component	Shipping	Storage
820-00017	AVITI 2x300 Cartridge Cloudbreak Medium Output	-25°C to -15°C	-25°C to -15°C
810-00002	AVITI Flow Cell Cloudbreak	Room temperature	2°C to 8°C
820-00010	Adept Primer Set Cloudbreak	-25°C to -15°C	-25°C to -15°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

Adept Primer Set Cloudbreak

Primers for I1, I2, R1, and R2 provided in Cloudbreak cartridges support Elevate libraries. Sequencing Adept libraries requires replacing the prepackaged primers with tubes from the Adept Primer Set Cloudbreak.

Adept Primer Set Cloudbreak, catalog # 820-00010

- Index 1—Adept Index 1 (I1) Primer Cloudbreak
- Index 2—Adept Index 2 (I2) Primer Cloudbreak
- Read 1—Adept Read 1 (R1) Primer Cloudbreak
- Read 2—Adept Read 2 (R2) Primer Cloudbreak

The Adept Primer Set Cloudbreak is not compatible with Cloudbreak Freestyle or Cloudbreak UltraQ kits.

PhiX Control Library

PhiX Control Library is a color-balanced, ready-to-use library that adds diversity to low-complexity libraries. Each type of PhiX Control Library includes unique index sequences and has a concentration of 1 nM. For a list of sequences, see *Element Index Sequences*.

Type	Format	Shipping and Storage
PhiX Control Library, Adept, # 830-00004	Circular	-25°C to -15°C
Cloudbreak PhiX Control Library, Elevate, # 830-00017	Linear	-25°C to -15°C
Cloudbreak Freestyle PhiX Control, Third Party, #830-00023	Linear	-25°C to -15°C

Custom Primer Sets

A custom primer set provides read-specific buffers for preparing custom primers for Adept libraries with Cloudbreak chemistry or third-party libraries with Cloudbreak Freestyle chemistry.

Custom Primer Set	Buffers	Shipping and Storage
Adept Custom Primer Set Cloudbreak, # 820-00009	• Adept Custom Index 1 Buffer, Index First (I1) • Adept Custom Index 2 Buffer, Index First (I2) • Adept Custom Read 1 Buffer, Index First (R1) • Adept Custom Read 2 Buffer, Index First (R2)	-25°C to -15°C
Custom Primer Set Cloudbreak Freestyle, # 820-00025	• Custom Index 1 (I1) Buffer Cloudbreak Freestyle • Custom Index 2 (I2) Buffer Cloudbreak Freestyle • Custom Read 1 (R1) Buffer Cloudbreak Freestyle • Custom Read 2 (R2) Buffer Cloudbreak Freestyle	-25°C to -15°C

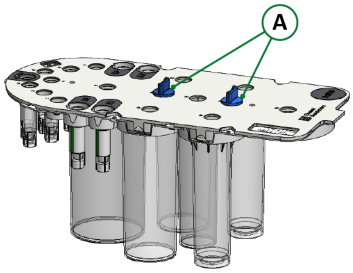
User-Supplied Consumables and Equipment

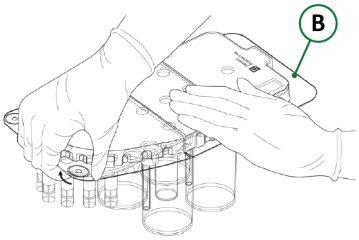
Consumables	Supplier
DNA LoBind Tubes, 2 ml	Eppendorf, # 022431021
0.2 M Tris-HCl, pH 7.0	General lab supplier
1 N NaOH	
10 mM Tris-HCl, pH 8.0 with 0.1 mM EDTA	
Filtered pipette tips	
Low TE buffer	
Nuclease-free laboratory-grade water	

Cartridge Shipping Configuration

The Cloudbreak sequencing cartridge includes shipping protection in the form of shipping locks or a thermoform shipping cover.

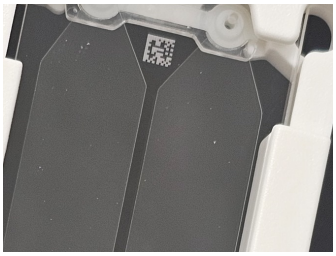
- If your cartridge includes the shipping locks (**A**), remove the shipping locks before loading the cartridge onto the instrument.
- If your cartridge includes the thermoform shipping cover (**B**), remove the cover before thawing reagents.





Cloudbreak Flow Cell Variations

Cloudbreak flow cells might have small particulate within the flow cell lane. These variations are normal and do not impact data quality.



Document History

Revision	Description of Change
April 2025 Document # MA-00058 Rev. E	• Updated expected priming time when using AVITI OS v3.3.
March 2025 Document # MA-00058 Rev. D	• Added run times for each kit configuration. • Added Read Counts and Outputs table to Overview section. • Added Universal Wash Buffer to each mention of AVITI Buffer Bottle. • Removed the term pollination in the Run Stages description. • Updated storage time for thawed cartridges.
January 2025 Document # MA-00058 Rev. C	• Added recommendations for using short insert and long insert recipes. • Added run specifications for the Cloudbreak Freestyle 2 x 75 low output kit. • Added example of different cartridge shipping configurations, such as shipping locks or shipping cover. • Added statement that Cloudbreak flow cell variations do not impact data quality. • Recommended a pipette tip or similar tool to enlarge hole in foil seal.
December 2024 Document # MA-00058 Rev. B	• Added 2 x 75 Cloudbreak Freestyle Low Output kit. • Updated name of sequencing basket to cartridge basket.
October 2024 Document # MA-00058 Rev. A	• Initial release of user guide.

Technical Support

Visit the Documentation page on the Element Biosciences website for additional guides and the most recent version of this guide. For technical assistance, contact Element Technical Support.

Website: www.elementbiosciences.com

Email: support@elembio.com

Telephone: +1 866.ELEMBIO (+1 866.353.6246)

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EXHIBIT 14

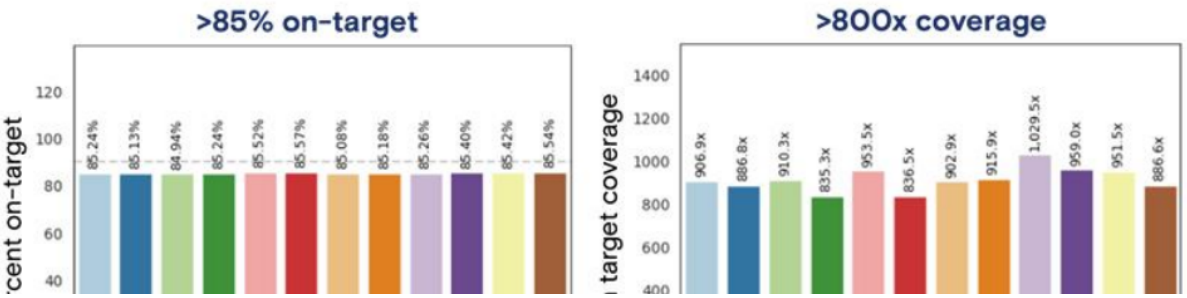
Cloudbreak™ Sequencing Kits

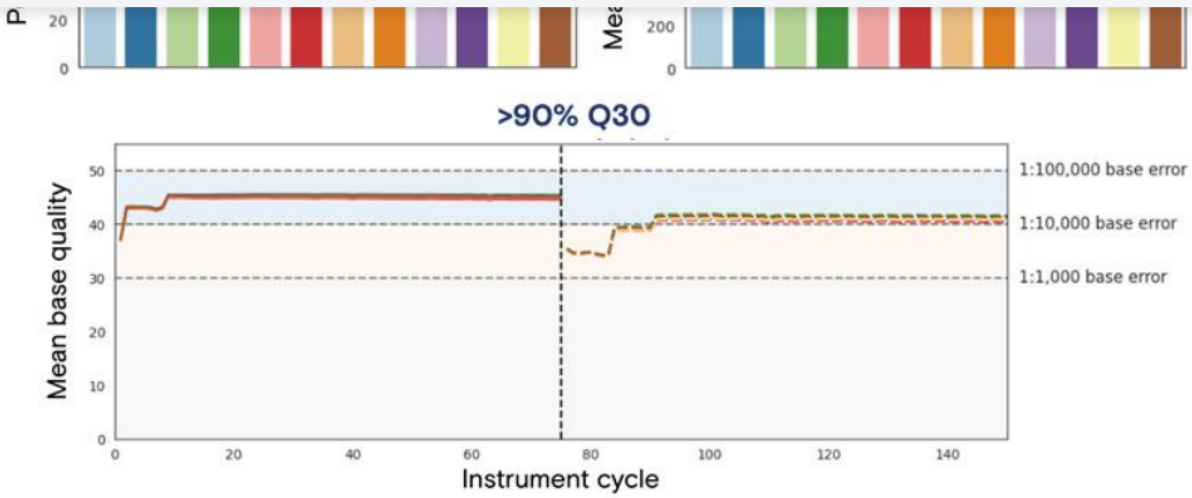
Cloudbreak sequencing kits provide the sequencing reagents and flow cell for a run on the Element AVITI™ System with multiple read lengths and output options to suit any application. Leveraging avidite base chemistry (ABC), Cloudbreak kits deliver simplified workflows and Q50 data quality (with UltraQ™) with low costs and rapid turnaround times.

Watch Video >
Product Compatibility >
Compare Data >

Powerfully flexible

Cloudbreak sequencing kits enable a range of applications and scale for experiments of any size. Comprehensive sequencing kits run any read length from 2 x 75 to 2 x 300 with low-, medium-, and high-output kits allowing you to dial in a precise number of reads while maintaining affordability.



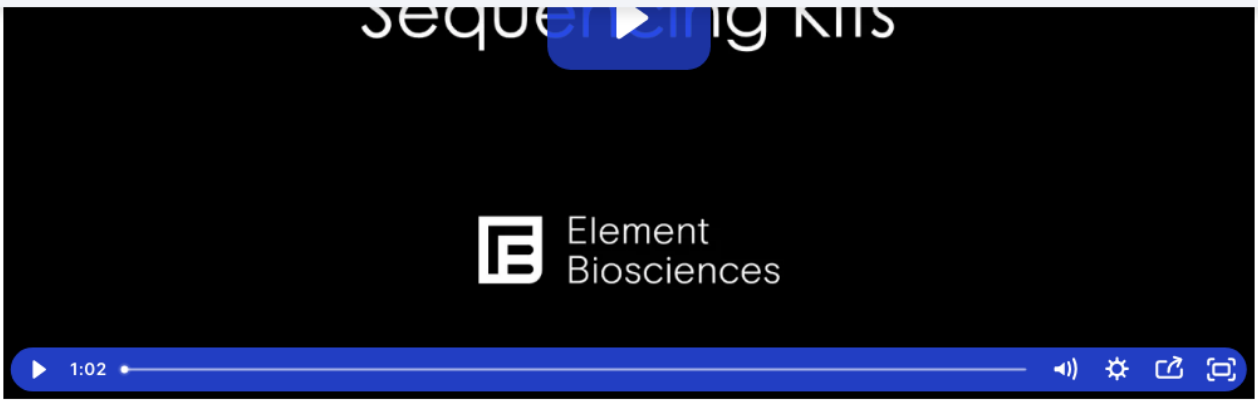


If your application requires low output, you can run your samples immediately with 2 x 75 low output kits—no need to wait to batch them. Leverage faster turnaround and the lowest run cost to get to your data faster.

Simplified workflows and seamless compatibility

Cloudbreak Freestyle™ kits simplify your AVITI sequencing workflow like never before. By enabling linear library loading and circularization onboard the AVITI System, Cloudbreak Freestyle eliminates the library conversion step, saving valuable preparation time and ensuring seamless integration with your existing library prep workflows.

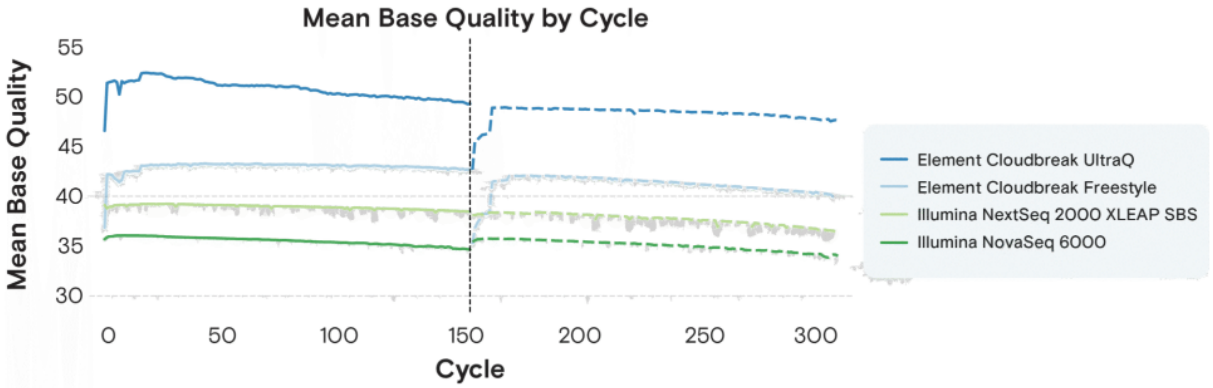
Learn more about Cloudbreak Freestyle >



Setting a new standard: Q50+ data quality

Cloudbreak UltraQ sets a new standard for sequencing accuracy, pushing the potential of the AVITI system even higher. With the highest accuracy specification on the market today, UltraQ delivers 70% of reads at Q50 or above and 90% of reads at Q40 or above. By using multiple strategies to reduce the most abundant error types arising from library prep and sequencing, it provides the firmest possible foundation for the development of highly sensitive assays.

Discover UltraQ >



Included in Each Kit

- **Flow cell** encased in a plastic cartridge for safe handling.
- **Cartridge** that conveniently packages sequencing reagents.
- **Buffer bottle** that supplements the cartridge with a large buffer volume.
- **Library loading buffer** to dilute libraries to the target loading concentration.
- **Adept™ primer set** that provides primers compatible with Adept libraries (original Cloudbreak kits only).

Catalog Numbers

Name	Catalog #	Number of Cycles	Number of Reads*	Output (Gb)
Cloudbreak UltraQ (CB UltraQ) Kits				
AVITI 2x150 Sequencing Kit CB UltraQ	860-00018	323	800 million	240
Cloudbreak Freestyle (FS) Kits				
AVITI 2x75 Sequencing Kit Cloudbreak FS Low Output	860-00034	184	100 million	15
AVITI 2x75 Sequencing Kit Cloudbreak FS Medium Output	860-00014	184	500 million	75
AVITI 2x75 Sequencing Kit Cloudbreak FS High Output	860-00015	184	1 billion	150

AVITI 2x150 Sequencing Kit Cloudbreak FS Low Output	860-00011	334	250 million	75
AVITI 2x150 Sequencing Kit Cloudbreak FS Medium Output	860-00012	334	500 million	150
AVITI 2x150 Sequencing Kit Cloudbreak FS High Output	860-00013	334	1 billion	300
AVITI 2x300 Sequencing Kit Cloudbreak FS Medium Output	860-00016	634	100 million	60
AVITI 2x300 Sequencing Kit Cloudbreak FS High Output	860-00017	634	300 million	180
Cloudbreak Kits				
AVITI 2x75 Sequencing Kit Cloudbreak Medium Output	860-00007	184	500 million	75
AVITI 2x75 Sequencing Kit Cloudbreak High Output	860-00004	184	1 billion	150
AVITI 2x150 Sequencing Kit Cloudbreak Low Output	860-00005	334	250 million	75
AVITI 2x150 Sequencing Kit Cloudbreak Medium Output	860-00006	334	500 million	150
AVITI 2x150 Sequencing Kit Cloudbreak High Output	860-00003	334	1 billion	300
AVITI 2x300 Sequencing Kit Cloudbreak Medium Output	860-00009	634	100 million	60
AVITI 2x300 Sequencing Kit Cloudbreak High Output	860-00008	634	300 million	180
Accessory Kits				
PhiX Control Library, Adept	830-00004			
Cloudbreak PhiX Control Library, Elevate	830-00017			
Cloudbreak FS PhiX Control, 3rd Party	830-00023			

*Performance metrics, including read counts, are based on sequencing Element-prepared libraries. Actual results might differ based on factors such as library type and preparation.

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Resources

AVITI Documentation

ABC for NGS: How to Lower Costs and Raise Quality

Blog Post: Embracing the Library Prep Paradox

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EXHIBIT 15

Element Biosciences

Shift your science

AVITI™ gives scientists the freedom to unleash creativity and accelerate discovery for biological insights

Your engine for genomic innovation

The Element AVITI System reimagines next-generation sequencing (NGS) to bring affordable, world-class sequencing capability to all labs. This benchtop instrument upends establishment models with boundless scalability and the dynamism to expand into cellular profiling.

A low-throughput model, the Element AVITI System LT, further lowers the barrier to NGS entry with access to the same groundbreaking technology at a lower instrument cost.

Flexibility
Access applications with short- and long-read sequencing.

Affordability
Accelerate timelines with per-run costs that erase large batching.

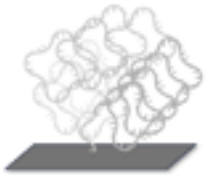
Performance
Distinguish true variants from errors with accurate, reliable data.

As elemental as ABC

Avidite base chemistry (ABC) leverages the power of avidites and PCR-free library amplification to define an entirely unique approach to sequencing. From scarless DNA to reduced wasted reads due to index hopping and optical duplication, ABC redefines what high-quality and low-cost sequencing can mean.

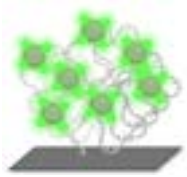
Circularization

A DNA library molecule attaches to low-binding surface chemistry coating the flow cell. A capture primer immobilized to the coating joins the library ends to circularize the DNA library molecule and prepare for PCR-free amplification.*



Amplification

Rolling circle amplification (RCA) copies the circularized DNA library molecule, creating a continuous strand bound into a polony. Only the circularized DNA library molecule is copied, neutralizing PCR artifacts to replicate DNA without distortion.

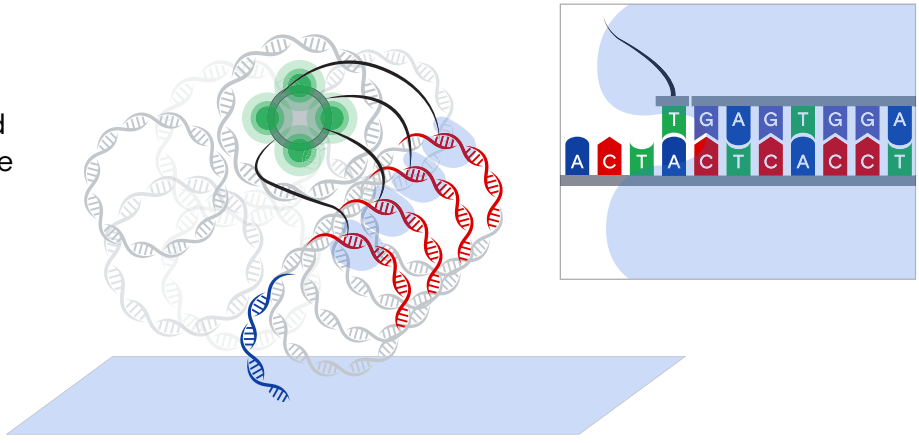


Sequencing

Avidites bind to the polony at multiple sequencing sites, creating a stable complex for imaging. Ultratight binding ensures signal persitance for precision base calling with a 100-fold reduction in reagent concentration.

Anatomy of a polony during sequencing

A polony is a continuous DNA strand that is bound with avidites at multiple sites during sequencing.



* RCA can also amplify manually circularized libraries.

Go further with Q50+

High quality delivers more usable data and improves sensitivity for variant detection and other applications that require accuracy. The quality benchmark is Q30. With Cloudbreak Freestyle™ routinely exceeding Q40 and Cloudbreak UltraQ™ delivering ≥70% of reads at Q50 and ≥90% of reads at Q40, AVITI sequencing sets a new standard for sequencing accuracy.

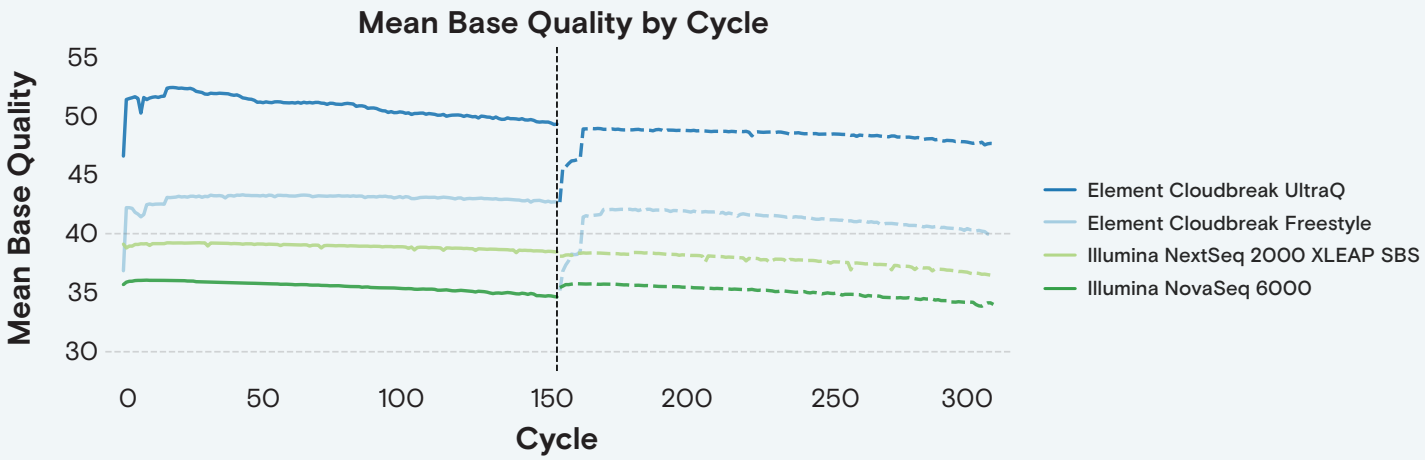


Figure 1. AVITI maintains Q30–Q50+ base quality even through the challenging sections at the ends of 150 bp reads.[1]

The standout quality of AVITI data is also evident in difficult, mutation-rich hotspots. RCA strengthens accuracy from the start by minimizing errors introduced through template amplification. Optimized enzymes and bioinformatics methods drive data to high-accuracy completion.

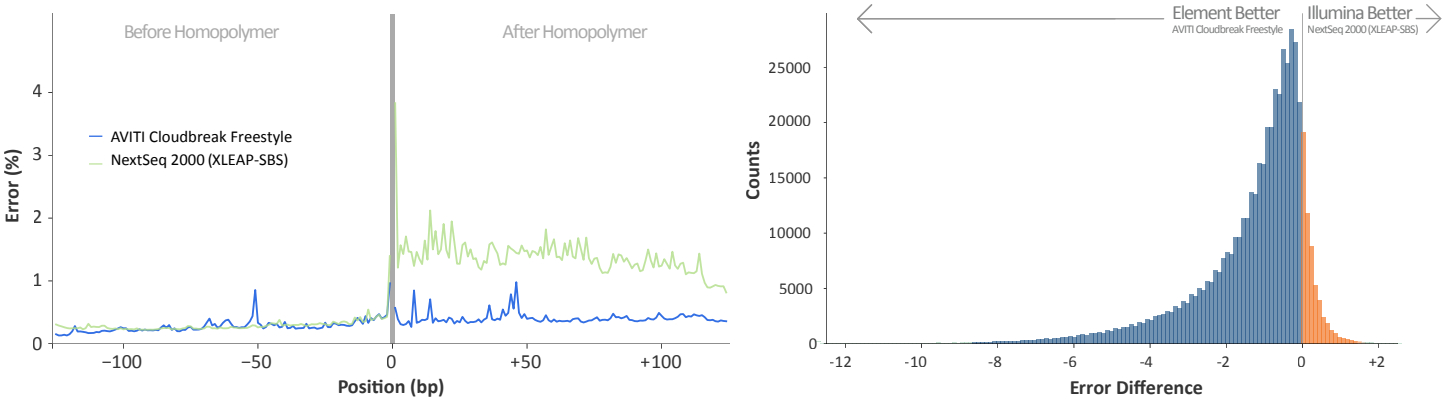


Figure 2. The AVITI error rate remains low following a long homopolymer (> 11 bp) while other systems suffer an average 3-fold increase (left). This performance extends across the majority of long homopolymers in the human genome (right).

Plug in any library prep

Extensive partnerships with third-party library prep providers let researchers craft an end-to-end solution that fits any need, starting with a choice of library prep. Maintain a current prep for AVITI sequencing or leverage the Element Elevate Library Prep Workflow to stay with Element Biosciences end-to-end.

Elevate™ Workflow

Prepare Element libraries from DNA input.

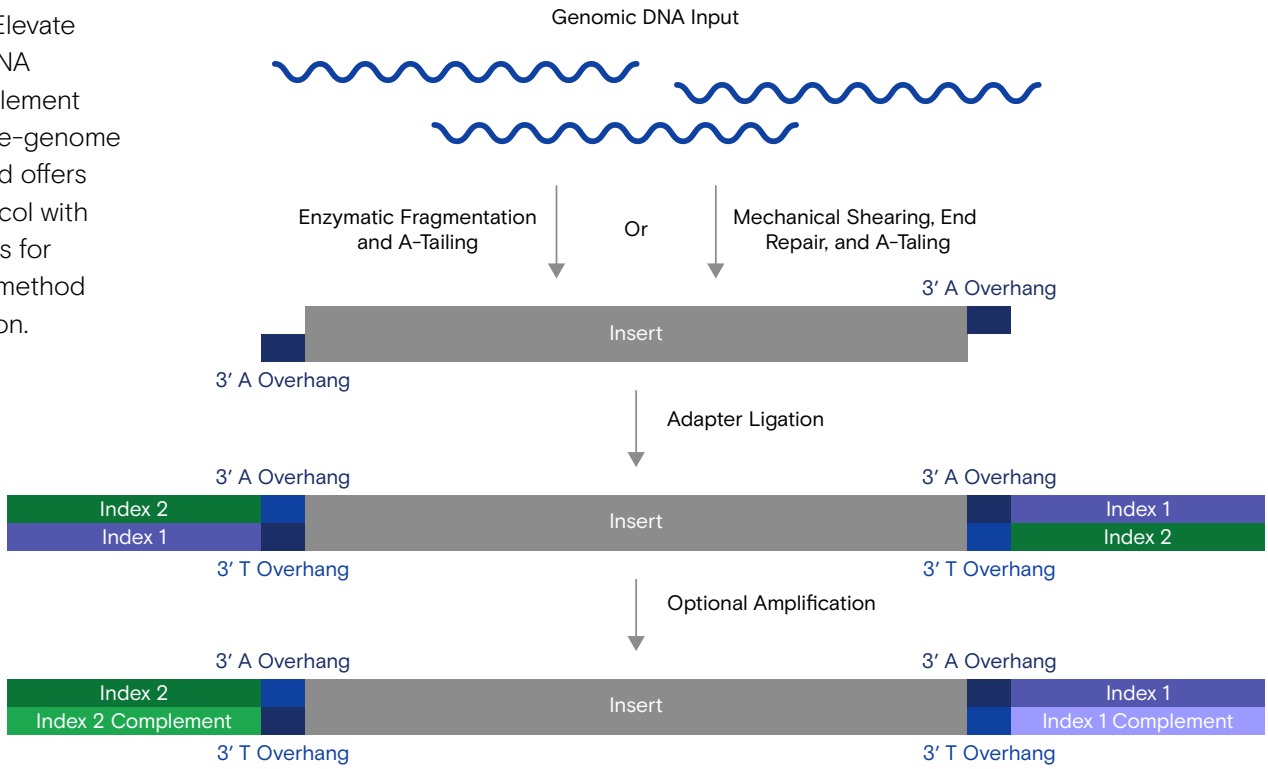
Adept™ Workflow

Adapt third-party libraries via circularization or amplification.

Third Party

Prepare third-party libraries from DNA or RNA input.

Figure 3. The Elevate Workflow for DNA generates an Element library for whole-genome sequencing and offers a flexible protocol with multiple options for fragmentation method and amplification.



Simple

Familiar library prep reagents and procedures deliver easy, efficient workflows.

Adaptable

Multiple library prep solutions equal multiple entry points to capitalize on AVITI benefits.

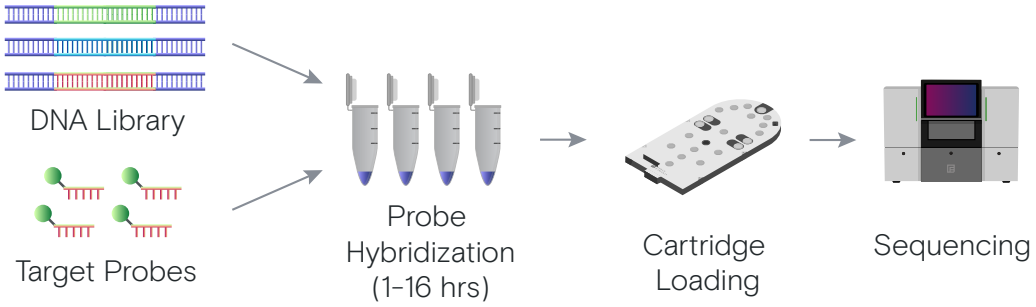
Compatible

ABC maximizes compatibility, streamlining AVITI sequencing for a diversity of library types.

Revolutionize your targeted sequencing workflows

Drastically simplifying target capture, our Trinity™ workflow saves up to 5 hours of hands-on time by eliminating some steps and automating others on board an AVITI sequencer, without compromising quality or cost.

Element Trinity Workflow



Tune your workflow

AVITI sequencing kits are packaged in configurations that tailor runs to your ideal read length and output. Generate only the number of reads you need at a price point that scales to match.

Each kit contains

- ✓ Flow cell
- ✓ Sequencing cartridge
- ✓ Buffer bottle
- ✓ Library loading buffer

Individually addressable lanes

Provides the option to sequence a different library pool in each of the two flow cell lanes.

Any application you need

Overarching compatibility with any NGS library meets a comprehensive menu of sequencing kits to unlock the full scope of sequencing applications. Whether you need 100 million reads or 2 billion, a short read length or long, AVITI is the solution.

Software that gets you to a result

Element software is simple, secure, and transparent. From onboard to in the cloud, Element lets users easily create end-to-end solutions through an open ecosystem, bringing flexibility and ease to NGS data management.

Figure 4. Interlocked components seamlessly move data from AVITI to FASTQ files for secondary analysis using software of your choice.

ElemBio™ Cloud

ElemBio Cloud is an online platform that centralizes data management. Innovative and user-friendly, ElemBio Cloud matches any lab to an analysis solution, scaling from plug-and-play simplicity to fully customized and self-managed.

Ground your analysis solution in a local network or pick from a range of cloud options.

ElemBio Go

Leverage an automated data storage and management solution for data flows in ElemBio Cloud through ElemBio Catalyst or a partner service.

ElemBio Custom

Select at least one cloud provider to develop a customized ecosystem for data analysis built on a cloud account that you manage.

ElemBio Local

Set up a custom local solution with offered utilities.

Element Biosciences

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[1] Comparative data derived from analyses of HG001 (Element Freestyle and Illumina datasets) and HG002 (Element UltraQ) benchmarks. Actual results might differ based on lab-specific factors.

EXHIBIT 16

Element Biosciences

Trinity™ Sequencing

User Guide

FOR USE WITH

AVITI™ System, catalog # 880-00001
AVITI24™ System, catalog # 880-00004
AVITI Operating Software v3.3.0 or later
Trinity Sequencing Kits

ELEMENT BIOSCIENCES
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Document # MA-00059 Rev. C
April 2025

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Table of Contents

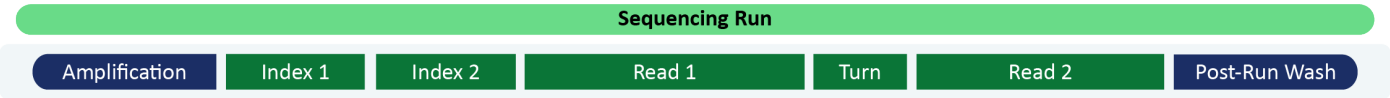
Overview

This guide provides instructions for performing a Trinity sequencing run using libraries prepared from a Trinity hybridization reaction.

Sequencing Run Stages

AVITI Operating Software (AVITI OS) generates a recipe based on the run parameters entered during run setup. The recipe governs each stage of a run. A run is complete when the recipe is executed and primary analysis is finished. The following stages comprise a sequencing run:

- **Amplification**—Hybridizes the library to the flow cell and performs amplification to form polonies, each containing multiple copies of the same sequence from the library.
- **Sequencing**—Performs each read in the run, including imaging and primary analysis.
- **Post-run wash**—Automatically flushes buffer from the sequencing cartridge through the fluidic system to remove salts and residual library.



Reads in a Sequencing Run

Up to four reads comprise a sequencing run: Index 1, Index 2, Read 1, and Read 2.

- **Index reads**—A run can include one or two index reads.
  - » **Index 1** sequences the Index 1 sequence.
  - » **Index 2** sequences the Index 2 sequence.
  - » A dual-index run sequences Index 1 and Index 2.
- **Read 1 and Read 2**—All runs must have a Read 1.
  - » **Read 1** sequences the forward strand of the DNA insert.
  - » **Read 2** sequences the reverse strand.
  - » A paired-end run sequences Read 1 and Read 2, including a paired-end turn before Read 2 to generate the complementary strand.

Number of Cycles

Read length is the total number of cycles performed in a run. The optimal number of cycles and how to distribute the total cycles depends on your experiment. For bioinformatics purposes, adding one extra cycle to each read is recommended. For example, a 2 x 150 cycle run ideally includes 2 x 151 cycles. The additional cycle improves the accuracy of the Q score for the 150th cycle.

The software and chemistry used for the run prescribe a minimum number of cycles. Read 1 requires at least five cycles and at least 25 cycles to generate all run metrics. The maximum number of cycles depends on the kit:

- A 2 x 75 kit performs up to 184 cycles, supporting one 2 x 76 run with indexing and unique molecular identifiers (UMIs).
- A 2 x 150 kit performs up to 334 cycles, supporting one 2 x 151 run with indexing and UMIs.

Trinity Sequencing Kits

The Trinity workflow requires a Trinity sequencing kit to sequence the hybridized reaction on an AVITI™ or an AVITI24™ System. Each kit includes a flow cell, a buffer bottle, a reagent cartridge, the library loading buffer, and the Trinity sequencing reagent.

NOTE
The fast hybridization workflow requires the Trinity Fast Hyb Loading Buffer, catalog # 830-00030, in place of the library loading buffer.

Trinity kits are available in two sizes: a 2 x 75 kit and a 2 x 150 kit. See *Trinity Sequencing Kits* on page 15.

Trinity PhiX Control

A Trinity PhiX Control, catalog # 830-00031, is available as an optional spike-in for the sequencing run. The addition of the PhiX control is a valuable tool for quality control in the sequencing process, as it provides an error rate estimation for the run. Without the PhiX control, no error rate data are available for the sequencing run. See *Add Sequencing Solution to the Cartridge* on page 10.

Additional Documentation

For end-to-end workflow instructions including library preparation, see the following protocol guides:

- xGen Exome Sequencing Kit Trinity for Element AVITI System (MA-00056)
- Twist for Element Exome 2.0 + Library Preparation and Standard Hybridization With Trinity Sequencing Workflow (MA-00054)
- Twist for Element Exome 2.0 + Library Preparation and Fast Hybridization With Trinity Sequencing Workflow (MA-00055)

For experienced user documentation for the hybridization and run setup steps, see the following quick guides:

- xGen Exome Hybridization & Trinity Run Setup Quick Guide (MA-00061)
- Twist Exome Hybridization & Trinity Run Setup Quick Guide (MA-00064)
- Twist Exome Fast Hybridization & Trinity Run Setup Quick Guide (MA-00065)

Trinity Workflow Summary

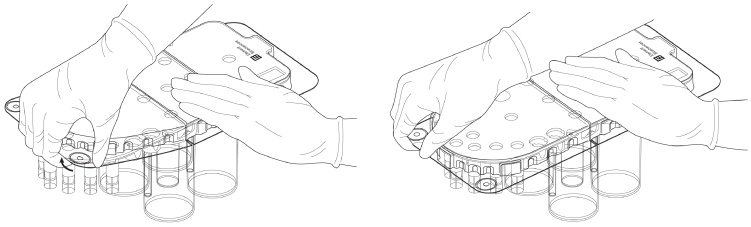
Preparing for a Trinity sequencing run includes steps to prepare a standard hybridization reaction or fast hybridization reaction. For hybridization protocols, see *Additional Documentation* on page 5.

Following the hybridization step, run setup includes steps to prepare the sequencing solution and add it to the reagent cartridge before loading consumables onto the instrument.

Thaw Reagents

1. Remove the shipping cover:

   a. While supporting the cartridge, lift the removal tab at the left corner until it releases from the cartridge.



   b. Moving across the front edge of the shipping cover, repeatedly lift the edge until the cover is fully released.

   c. Pull to remove the remainder of the shipping cover from the cartridge.

2. Thaw the Trinity sequencing cartridge. Protect the cartridge from light until loading onto the instrument.

Cartridge	Room Temperature Water Bath	Refrigerator
2 x 75	90 minutes	8 hours
2 x 150	2.5 hours	24 hours

3. Make sure reagents are *fully* thawed. Inspect each well as reagents thaw at varying rates.
4. If any ice remains, continue thawing.
5. Set aside the thawed cartridge at room temperature. If you do not immediately initiate the run, place the thawed cartridge at 2°C to 8°C. You can store overnight for use the next day.
6. Proceed to *Run Setup* on page 8.

Run Setup

Run setup for sequencing prompts you to define run parameters, load sequencing consumables, and empty the waste bottle. Before initiating a run, review the overview, software, troubleshooting, and safety information in the user guide for your instrument.

Initiate a Sequencing Run

1. Gather the following materials:
   - » Buffer bottle
   - » Cartridge
   - » Cartridge basket
   - » Towel or wipe
   - » Used flow cell

   —A used flow cell might already be present on the instrument.—
2. If applicable, stage run manifests for import:
   - » If setting up the run manually, save the manifest on a USB and connect the USB drive to an instrument USB port.
   - » Alternatively, you can save the manifest to the specified SMB storage connection.
   - » If you planned the run in Elembio Cloud, upload the manifest to the planned run.
3. On the Home screen, select **New Run**.
4. If AVITI OS prompts that the flow cell is missing, load a ***used*** flow cell:
   a. Select **Open Nest**.
   b. Place the used flow cell onto the nest and close the lid.
   c. Select **Close Nest**.
5. Select **Sequencing**.
6. Select the side for sequencing:
   - » **Side A**—Set up a run on side A.
   - » **Both**—Set up runs on sides A and B.
   - » **Side B**—Set up a run on side B.
7. For chemistry type, select **Trinity**, and then select **Next**.
8. Proceed as follows:
   - » For a planned run created in Elembio Cloud, proceed to *Select a Planned Run*.
   - » For a manual run, proceed to *Define Manual Run Parameters* on page 9.

Select a Planned Run

1. Select **Planned Run**.

   AVITI OS displays a list of compatible planned runs for the instrument and run type. For information on planned run compatibility, see *Run Planning* in the *Online Help*.
2. Select the run you want to use from the list of planned runs.
3. Review the run parameter fields to make sure they are correct.

   If you need to edit a planned run, modify it in Elembio Cloud. See *Run Planning* in the *Online Help*.
4. In the Storage drop-down menu, select the storage connection for the run.

5. Select **Next** to proceed to the Prepare Reagents or the Run Side B screen.
   - » After you proceed, the selected planned run becomes unavailable for other connected instruments.
   - » If you exit run setup before priming, the run returns to the list of available planned runs.
6. If applicable, repeat steps 2–5 to set up a dual start run with a second planned run.
7. Proceed to *Inspect and Mix Reagents* on page 10.

Define Manual Run Parameters

1. Make sure **Manual Run** is selected for the type of run.
2. In the Run Name field, enter a unique name to identify the run.

   —The field accepts 1–64 alphanumeric characters, hyphens (-), and underscores (_).—
3. If applicable, select **Browse** and import the run manifest.
4. [Optional] In the Description field, enter a description that represents the run.

   —The field accepts ≤ 500 alphanumeric characters, hyphens, underscores, spaces, and periods (.).—
5. In the Storage drop-down menu, select a storage location:
   - » To output run data to the default storage location, leave the default selection.
   - » To override the default storage location for the current run, select a storage connection.
6. In the Sequencing Kit drop-down menu, select the Trinity sequencing kit you are using.
7. In the Panel drop-down menu, select one of the following panels:
   - » **Twist for Element, Trinity Exome Workflow**—For use with either the standard or fast hybridization protocols.
   - » **xGen Exome Kit for Trinity**—For use with the xGen Exome hybridization protocol.
   - » **Other**—For use with other panels not listed.

   NOTE
   When you select a panel, the standard bed file is copied to the run output folder for downstream analysis.
8. In the Cycles fields, enter the number of cycles to perform in each read.
   - » Do not exceed the maximum number of cycles for the sequencing kit. See *Number of Cycles* on page 4.
   - » Add one cycle to the number of Read 1 and Read 2 cycles. For example, enter **151** in the Read 1 field to perform 150 cycles.

Kit Size	Index 1	Index 2	Read 1	Read 2
2 x 75	12	9	76	76
2 x 150	12	9	151	151

9. If you are using the Advanced Run Settings add-on, select **Advanced Settings** and proceed to *Configure Advanced Run Settings*.
10. Select **Next** to proceed to Run Side B and repeat steps 2–10 or proceed to the Prepare Reagents screen.

Configure Advanced Run Settings

Use Advanced Run Settings to modify primary analysis and recipe configurations for a run. Available settings depend on kit compatibility. Some settings require the activation of an add-on. For more information, see the Advanced Run Settings and Add-On information in the user guide for your instrument.

1. If you are using the Polony Density setting, select a Polony Density option.
   - » **Standard**—Uses the standard read output.
   - » **High Density**—Increases the read output.

2. If you are using the Filter Mask setting, enter a base mask to use for filtering.
   - » Use the base mask format. For more information, see *Base Masks* in the *Online Help*.
   - » If you do not use the Filter Mask setting, the default filter mask is `R1:Y15N*-R2:Y15N*`.
3. If you are using the Custom Recipes setting, import the custom recipe file from preloaded recipes or a USB drive:
   a. Select **Browse**.
   b. Select **Element Recipes** for preloaded recipes or **USB** to upload from a connected USB drive.
   c. Select the recipe file, and then select **Open**.
4. Select **Next** to proceed.

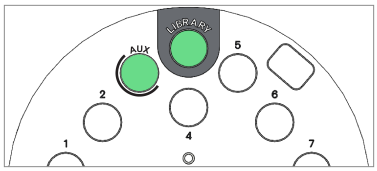
Inspect and Mix Reagents

1. Inspect each cartridge well to make sure reagents are fully thawed.
2. Make sure the cartridge contains the appropriate primers.
3. Make sure the tubes in the I1, I2, R1, and R2 wells are secure. If necessary, twist each tube to the right.
4. Gently invert the cartridge ***10 times*** to mix reagents.

   CAUTION
   Inadequately mixed reagents can cause run failure.
5. Tap the cartridge base on the benchtop to remove any large droplets from the tube tops.
6. Inspect the small tubes to make sure reagents are settled at the bottom.
7. Place the cartridge into a clean cartridge basket and lock the clips. Wipe any excess moisture.

Add Sequencing Solution to the Cartridge

1. Using a new 1 ml pipette tip, pierce the center of the Library well to create one hole. Push the foil to the edges.



2. Discard the pipette tip.
3. [Optional] Add 8 µl Trinity PhiX Control to the sequencing solution. Pipette gently to mix.

   Estimate a 0.5–5% representation in the Trinity sequencing run.
4. Transfer 2200 µl sequencing solution to the Library well, dispensing along the well wall.
   - » Avoid aspirating any foam or dispensing air.
   - » Do not allow the sequencing solution to contact the foil.
5. Inspect the Library well through the window at the front of the basket.
   - » Make sure the sequencing solution is free of foam and that bubbles are minimal.
   - » If an air gap appears below the surface, use a new pipette tip to remove it.

Confirm Reagent Preparation

1. Select the **Invert cartridge** checkbox to confirm that reagents are mixed.
2. Select the **Insert into basket** checkbox to confirm that the cartridge is in the cartridge basket.

3. Select the **Load hybed reaction** checkbox to confirm that the cartridge contains the hybridized reaction and sequencing solution.
4. Select **Next** to proceed to the Load Reagents screen.

Load Reagents and Buffer

1. Open the reagent bay door.
2. Remove any materials from the reagent bay and set aside.
3. Slide the basket containing the thawed cartridge into the reagent bay until it stops.
4. Support the buffer bottle with both hands and slide it into the reagent bay until it stops.
5. Close the reagent bay door, and then select **Next** to proceed.

Empty Waste and Prime Reagents

1. Open the waste bay door.
2. Unscrew the transport cap from the cap holder above the waste bay.
3. Remove the waste bottle from the waste bay and close the transport cap.

   CAUTION
   Waste bottle contents are considered hazardous. Dispose of waste according to local, state, and regional laws and regulations.
4. [Optional] Insert a funnel into a waste receptacle. Make sure the funnel is secure.
5. Open the transport cap and the vent cap.
6. Support the waste bottle with both hands and empty the waste:
   a. Position the bottle over the funnel or waste receptacle.
      - If you inserted a funnel, align the handle to the inner edge of the funnel.
      - If you did not insert a funnel, center the handle over the waste receptacle.
   b. Tip the bottle forward and drain. Invert the bottle and shake to expel all droplets.
   c. If necessary, wipe liquid off the bottle.
7. Close the vent cap and return the empty waste bottle to the waste bay.
8. Screw the transport cap onto the cap holder and close the waste bay door.
9. Bring a new Trinity flow cell to room temperature:
   a. Remove a flow cell pouch from 2°C to 8°C storage. ***Do not open the pouch.***
   b. Set aside the pouch for at least 5 minutes.

   NOTE
   Before priming, you can discard run setup and save the cartridge. Priming pierces reagent seals and prevents further use.
10. Select **Next** to ***automatically*** start priming.

    Priming takes ~ 5 minutes or up to 8 minutes at high elevations.
11. When priming is complete, select **Next** to proceed to the Load Flow Cell screen.

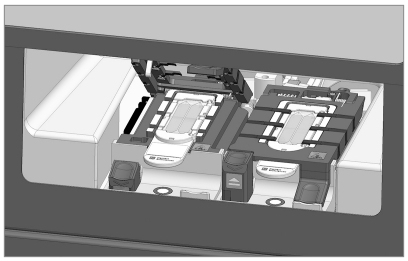
    AVITI OS moves the nest forward and opens the nest bay door. A brief delay is normal.

Load the Flow Cell

1. Make sure the nest status light is blue.

2. Press the button to the left of the nest to open the lid. Failure to fully press down on the button can cause errors when closing the lid or aligning the flow cell.
3. Remove the used flow cell from the nest. Discard or store at room temperature for use with priming or washes.
4. Unpackage the new Trinity flow cell. Handle the flow cell by the gripper only.

   CAUTION
   Touching the glass can introduce debris, smudges, and scratches, compromising data quality.
5. Face the label up and place the flow cell over the three registration pins on the nest.



6. Lower the tab on the right side of the lid until the lid snaps into place.
7. Select **Close Nest** to close the nest bay door and retract the stage.
8. Select **Next** to proceed to the Run Summary screen.

Review and Start the Run

1. On the Details page, review the run parameters:

Parameter	Description
Application	The type of sequencing application for the run
Library	The workflow that prepared the libraries and the library type
Sequencing Kit	The size and version of the sequencing kit
Storage	The location where sequencing output is stored
Manifest	The file name of the uploaded run manifest, if applicable
Panel	The panel for a Trinity workflow
Cycles	The number of cycles in each read
Description	An optional description of the run
Advanced	If applicable, the advanced run settings for the run

2. Review the flow cell, cartridge, and buffer bottle information:

Field	Description
Lot Number	The number assigned to the batch the consumable was manufactured with
Expires on	The year, month, and date that the consumable expires
Serial Number	The unique identifier or all zeros indicating an unscanned barcode
Part Number	The Element-assigned identifier for the consumable

3. Select **Run** to start sequencing.

4. [Optional] If you imported run manifests from a USB drive, disconnect the USB drive:
   a. In the taskbar, select **USB Drive**, and then select **Eject**.
   b. Detach the USB drive from the instrument.
5. Process the materials removed from the reagent bay:
   » For a used cartridge and buffer bottle, follow the instructions in *Discard the Cartridge and Bottle* on page 13.
   » For a wash tray, follow the guidelines in the user guide for your instrument. Residual liquid in the wash tray is normal.

Monitor Run Metrics

1. If necessary, select **Details** to open run details.
2. Monitor run metrics as they appear onscreen. AVITI OS indicates the expected cycle that metrics appear.
   —The expected cycles are approximate, and all metrics are estimates. Bases2Fastq generates the final metrics.—
3. Continue monitoring the run as AVITI OS refreshes the metrics.
   » Each cycle refreshes the Q scores, error rates, base compositions, and index metrics.
   » AVITI OS refreshes the yield and reads metrics after cycle 15 of Read 2:
      ◦ If Read 2 contains no cycles, metrics refresh after cycle 15 of Read 1.
      ◦ If Read 1 or Read 2 contain fewer than 15 cycles, metrics refresh when the last cycle begins.
4. When the run is complete, leave all materials on the instrument.
   » To return to the Details view, select **Overview**.
   » To access run data, go to your storage location.

Initiate Flexible Start

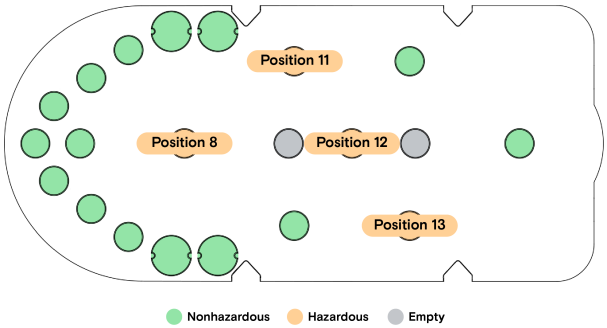
Flexible start provides the option to start a run or recovery wash while another run is in progress. AVITI OS safely pauses the run on the adjacent side.

1. On the Home screen, select **New Run**.
2. When prompted to request flexible start and pause the active run, select **New Run**.
3. Wait for the run to pause.
   » To cancel flexible start while waiting, select **Cancel Request**.
   » Contact Element Technical Support if the wait time exceeds 5 hours at the amplification step or 1.5 hours at any other step.
4. When the run pauses, proceed through run setup and start the second run or recovery wash.
   » For run setup instructions, proceed to *Initiate a Sequencing Run* on page 8.
   » For recovery wash instructions, see the user guide for your instrument.
5. To cancel setup of the second run or recovery wash, select **Back** to return to the Home screen, and then select **Resume**.

Discard the Cartridge and Bottle

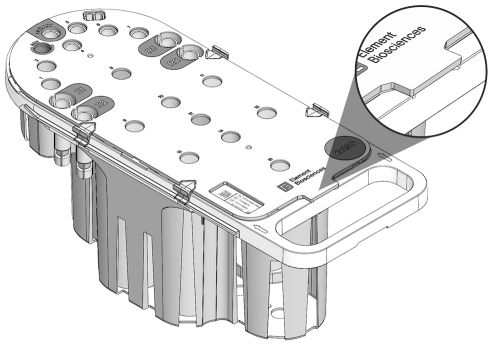
The cartridge and buffer bottle contain reagents with region-specific disposal requirements, which are described in the Safety Data Sheets (SDS) at elementbiosciences.com/resources. The amount of reagent remaining in each well after a run depends on how many cycles the run performed.

The following wells contain hazardous reagents. The position numbers in the figure align with the position numbers in the SDS.



Dispose of Reagents

1. Keep the cartridge in the basket with the clips locked.
2. Grip the lid tab and ***quickly and forcefully*** pull off the lid. Expect resistance.



3. Remove the wells indicated as hazardous from the cartridge.
   —The volume remaining in each well depends on the number of cycles performed.—
4. Using a pipette tip or a similar tool, enlarge the hole in each foil seal to form a triangle.

5. Empty each well into hazardous waste or other appropriate container per the SDS.
6. Unlock the clips and remove the cartridge from the basket.
7. Remove the remaining wells from the cartridge and enlarge the hole in each foil seal.
8. Empty each well into the appropriate container per the SDS.
9. Discard the cartridge and buffer bottle per the SDS.
10. Rinse the basket with nuclease-free water and dry upside down.

Trinity Sequencing Kits

The following tables list the kit contents and storage requirements for Trinity sequencing kits. Each kit is single-use and packaged in two boxes.

When you receive your kit, promptly store the components at the proper temperatures. For Safety Data Sheet (SDS) information, see elementbiosciences.com/resources.

Trinity 2x75 Sequencing Kit, # 860-00019

Part #	Component	Shipping	Storage
820-00030	Trinity 2x75 Cartridge	-25°C to -15°C	-25°C to -15°C
810-00015	Trinity Flow Cell	Room temperature	2°C to 8°C
830-00028	Trinity Sequencing Reagent	-25°C to -15°C	-25°C to -15°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

Trinity 2x150 Sequencing Kit, # 860-00020

Part #	Component	Shipping	Storage
820-00031	Trinity 2x150 Cartridge	-25°C to -15°C	-25°C to -15°C
810-00015	Trinity Flow Cell	Room temperature	2°C to 8°C
830-00028	Trinity Sequencing Reagent	-25°C to -15°C	-25°C to -15°C
820-00002	AVITI Buffer Bottle (Universal Wash Buffer)	Room temperature	Room temperature
820-00004	Library Loading Buffer	-25°C to -15°C	-25°C to -15°C

Trinity Binding Reagent, # 830-00029

Component	Storage
Trinity Binding Reagent	-25°C to -15°C

Trinity Fast Hyb Binding Reagent, # 830-00034

Component	Storage
Trinity Fast Hyb Binding Reagent	-25°C to -15°C

Trinity Fast Hyb Loading Buffer, # 830-00030

Component	Storage
Trinity Fast Hyb Loading Buffer	Room temperature

Trinity PhiX Control, # 830-00031

Component	Storage
Trinity PhiX Control	-25°C to -15°C

Document History

Revision	Description of Change
April 2025 Document # MA-00059 Rev. C	• Updated expected priming time when using AVITI OS v3.3. • Updated storage time for thawed cartridges. • Added Universal Wash Buffer to AVITI Buffer Bottle in kit component list. • Removed the term pollination in the Run Stages description.
January 2025 Document # MA-00059 Rev. B	• Corrected step in Dispose of Reagents to use a pipette tip or similar tool to enlarge hole in foil seal. • Added a link to the hybridization protocols on the workflow summary page.
December 2024 Document # MA-00059 Rev. A	• Initial release.

Technical Support

Visit the Documentation page on the Element Biosciences website for additional guides and the most recent version of this guide. For technical assistance, contact Element Technical Support.

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EXHIBIT 17

Trinity

Our Trinity workflow radically reimagines targeted sequencing workflows by eliminating or automating time-consuming steps onboard an AVITI™ system, saving up to 5 hours of hands-on time. Accelerate your time to discovery with improved library complexity and a reduction in risk of human error.

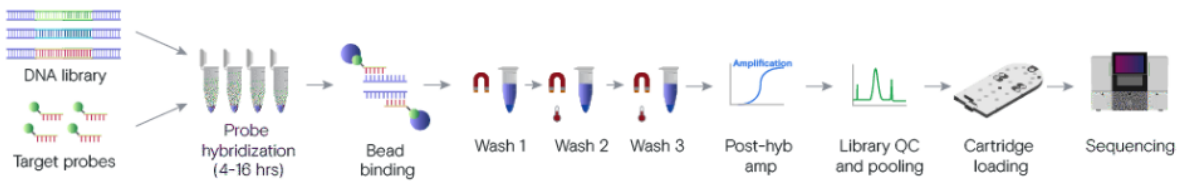
Download Infographic >
Explore Datasets >

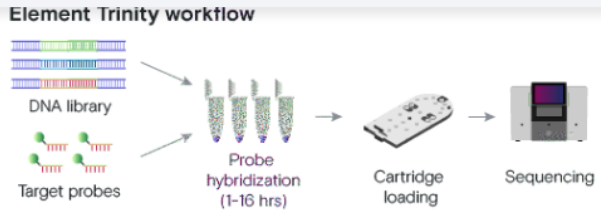
Revolutionary Workflow

The traditional hybrid selection process for targeted panels, like exomes, involves a time-consuming process with multiple temperature-controlled washes, PCR-based amplification, and library quality control.

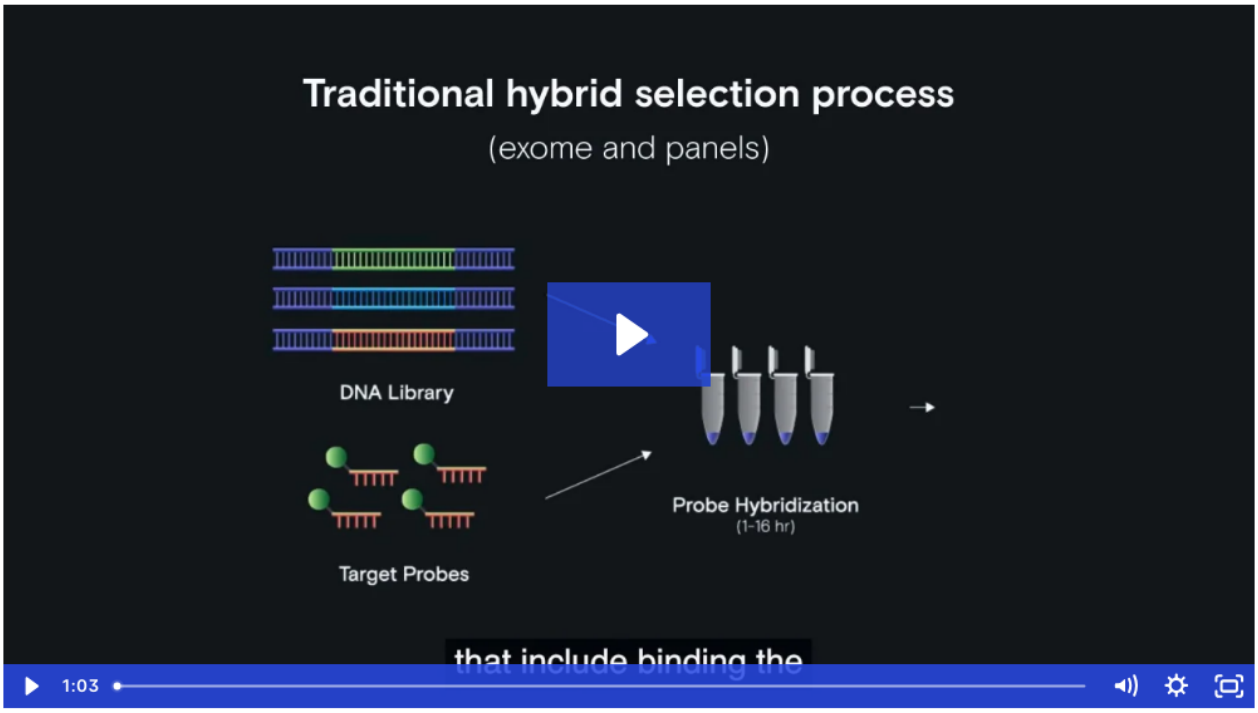
With the simplified Trinity workflow, you simply hybridize your DNA library to the target probes of interest, wait for the prescribed time, and load it directly onto an AVITI—drastically reducing manual steps and additional amplification resulting in higher library complexity and lower duplication rates.

Traditional hybrid selection process
(Exome and panels)





Learn more about the Trinity Workflow

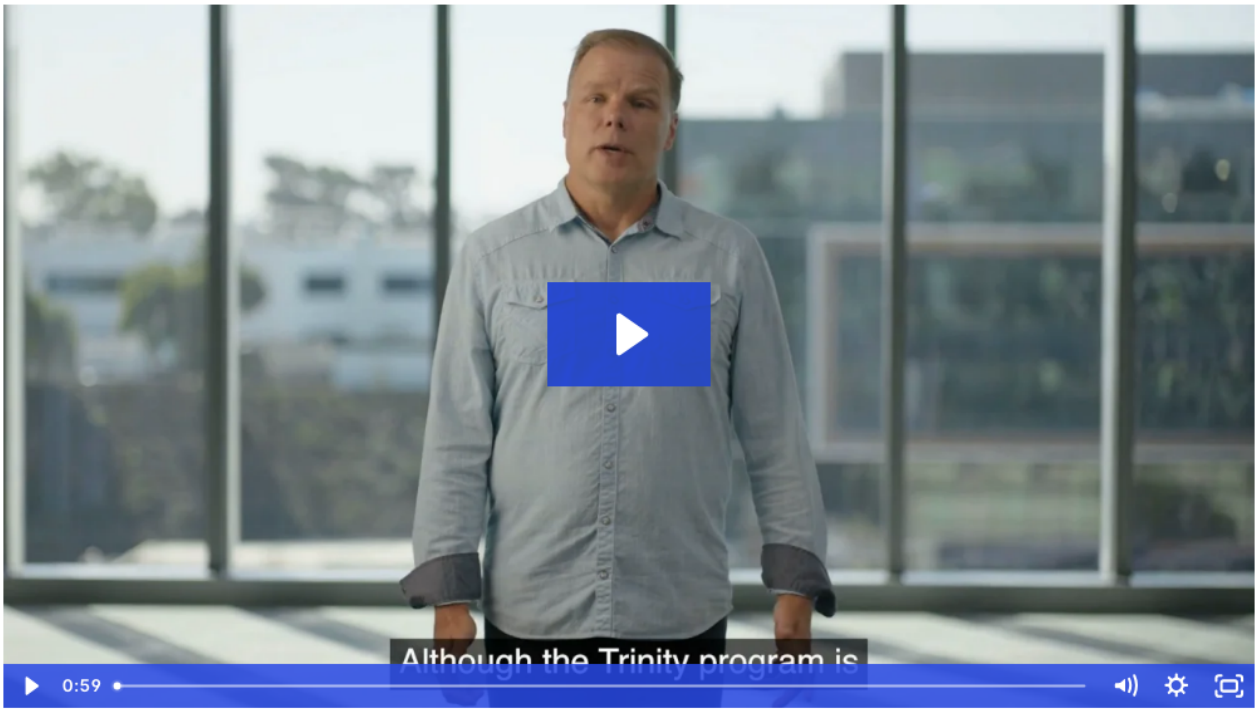


Compatible Panels

We have established supported workflows for exome sequencing applications in collaboration with Twist Bioscience and IDT. Trinity sequencing kits and binding reagents can be purchased directly from Element Biosciences while reagents for library preparation and hybridization can be purchased from either of our partners.

with panels ranging from hundreds to thousands of targets. Please contact us for additional guidance on running alternative panels.

Learn more about Trinity compatibility



Improved library complexity

Trinity not only improves the workflow of hybrid selection sequencing, it also improves performance with a dramatic reduction in duplication rate and higher library complexity when compared to libraries run in-solution. This allows for more efficient sequencing where we see higher coverage per sequencing read.

Download our infographic to see the data

Trinity sequencing kits are configured to sequence 24 exomes per flow cell with mean target coverage at ≥ 50x and the ability to scale the plexity depending on your coverage needs. For added TAT flexibility, Trinity is available in both 2 x 75 and 2 x 150 options.

Download Datasets >

View Documentation >

Performance Metrics

Quality	≥ 90% Q30
On-Target %	≥ 85%
Fold 80	Fold 80 ≤ 1.5
Run Time	2 x 75: 24 hours 2 x 150: 38 hours
Mean Target Coverage (24-plex)	2 x 75: ≥ 30x 2 x 150: ≥ 50x

Ordering Information

Element Biosciences	
Trinity 2x75 Sequencing Kit	860-00019
Trinity 2x150 Sequencing Kit	860-00020
Trinity Binding Reagent	830-00029
Trinity Fast Hyb Loading Buffer	830-00030
Trinity Fast Hyb Binding Reagent	830-00034
Trinity PhiX Control	830-00031
IDT*	

xGen Exome Sequencing Kit Trinity for Element	10022463
Twist Bioscience*	
Twist for Element Trinity, Exome 2.0 + Comp Spike, Standard Hyb Workflow	109326
Twist for Element Trinity, Exome 2.0 + Comp Spike, Fast Hyb Workflow	109327

*Please contact our partners directly to purchase these reagents.

Get in touch

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Last Name *
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Company Name *
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Select a State *
Zip Code
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Cancer
Product Interest
How Can We Help You?

☐ I would like to speak with an Element Specialist.

☐ I want to stay up-to-date with the latest Element news.

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